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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Novel tumor antigen protein ART-1, tumor antigen peptide originating from it, their derivatives, and DNAs, applicable in vivo or in vitro as remedies, preventives and diagnostics for tumors

Cenarchaeum symbio Cenarchaeum symbio Immunogenic peptid HIV peptide SEQ ID Human HIV-1 Th-CTL HIV peptide fragment o HIV Th-CTL peptide HIV TH-CTL peptide HIV TH-CTL epitope Human pancreatic C Human digestive sy Human digestive sy Human protein sequ H. Pylori outer me H. Pylori outer me H. Pylori outer me Human protein sequ Human protein sequ Human protein sequ Human polypeptide, Novel central nerv	00 at +1at
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## ALIGNMENTS

Human; tumour antigen protein; ART-1; HLA antigen; cytostatic; bound cytotoxic T cell; tumour; cancer; remedy; prevent; diagnose. Human ART-1 peptide fragment SEQ ID #5. AAB03883 standard; protein; 8 AA. (SUMU ) SUMITOMO PHARM CO LTD. (ITOH/) ITOH K. 98JP-0341253. 99WO-JP06682. 26-OCT-2000 (first entry) WPI; 2000-412318/35. Itoh K, Gomi S; WO200032770-A1 Homo sapiens. 01-DEC-1998; 30-NOV-1999; 08-JUN-2000. AAB03883; AAB03883 ID AABC 

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Matches
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                                                                                                                                                                                                    Included in the invention are polynucleotide sequences encoding the ART-I protein, and mutated ART-I proteins which when broken down intracellularly produce a tumour antigen peptide that can recognise HLA antigen and bound cytotoxic T cells. Antibodies which specifically recognise ART-I and its derivative peptides, are also included in the invention. ART-I exhibits cytostatic activity. The tumour antigen protein, tumour antigen peptide originating from it, their derivatives, and DNAs are applicable in vivo or in vitro as remedies, preventives and diagnostics for tumours.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present sequence represents a fragment of the ART-1 protein, used in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                       invention relates to a novel human tumour antigen protein, ART-1
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virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
viral infectious disease; ART-1; human.
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100.0%; Pred. No. 7.8e+05;
ive 0; Mismatches 0;
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                                                  59pp; Japanese.
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                                            Claim 11; Page 35;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence represents a fragment of the ART-1 protein, used in
DNA encoding IFNS) are useful in the manufacture of a medicament for inducing antigen-specific T cells in an individual who has been administered with AP (or DNA encoding AP) or vice versa. The medicament is useful for the treatment or prophylaxis of a tumor or a viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel tumor antigen protein ART-1, tumor antigen peptide originating from it, their derivatives, and DNAs, applicable in vivo or in vitro as remedies, preventives and diagnostics for tumors
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Pred. No. 7.8e+05;
Mismatches 0;
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100.0%; Pred. No. 7.8e+05;
iive 0; Mismatches 0;
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nes 8; Conservative
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                                                                                                            infectious disease.
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB03886;
                                                                                                                                                                 Sequence
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Best Local S
Matches 8
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1 LYQAVATI

AAG98646 standard; Protein; 363 AA. AAG98646

(first entry) 21-SEP-2001

Human cell death protective cDNA clone CNI-00714 ORF3 protein, SEQ:81.

Cell death protective; apoptosis; necrosis; human; drug screening; cell death-associated disorder; central nervous system disorder; psychiatric disorder; neurological disorder; ischaemia-related disorder; stroke; cerebral infarction; ischaemic encephalopathy; neurodegenerative disorder; Alzheimer's disease; Huntington's disease; Parkinson's disease; infection; meningitis; malaria; trypanosomiasis; vascular disease; opthalmological disorder; diabetic retinopathy; benign tumour; anaemia; gastrointestinal disorder; gastrittis; ulcerative colitis; liver disease; biliary cirrhosis; kidney disorder; glomerulonephritis; cystitis; endometricosis; endocrine disorder; Grave's disease; Hashimoto's thyroiditis; skin condition; dermatitis; urticaria; immune disorder; acquired immunodeficiency syndrome; AIDS. macular degeneration; hypertension; myocardial infarction; atherosclerosis; respiratory disorder; asthma; transgenic animal; chronic obstructive pulmonary disease; neoplastic condition; cancer;

Homo sapiens.

WO200145638-A2

28-JUN-2001

11-DEC-2000; 2000WO-US33547.

99US-0461697. 14-DEC-1999;

(COGE-) COGENT NEUROSCIENCE INC

Barney S, Thomas MB, Portbury SD, Puranam K, Katz LC; 3

N-PSDB; AAH84170, AAH84173. WPI; 2001-390297/41.

Novel protective sequence polynucleotides and polypeptides, used to identify modulators of their expression and activity, which are used in to treat central nervous system conditions, diseases and disorders -

Claim 1; Fig 6C; 325pp; English.

protect against cell death (i.e., apoptosis or necrosis). Sequences which protect against cell death (i.e., apoptosis or necrosis). Sequences AAH84132, AAH84132, AAH84126, AAH84256, AAH84265, AAH84281, AAH84132, AAH84132, AAH84132, AAH84132, AAH84132, AAH84135 and AAH84367 represent 10 full-length cDNA clones, while the remaining nucleic acid Sequences within the range given above represent the open reading frames (ORFS) of these CDNA clones. Sequences AAG98810-AAG98829 represent the polypeptides encoded by the cell death protective oRFs. The cell death protective cDNA clones are able to protective ORFs. The cell death protective cDNA clones are able to pathways when injected into a cell predisposed to or undergoing cell death. The cell death protective nucleic acids and polypeptides can be used in the diagnosis and treatment of disorders associated with cell death, and to screen for compounds which modulate their activity or a cell protective nucleic acids and polypeptides and antibody, a ribozyme, or an antisense molecule, can also be used to treat cell death-related diseases. Such diseases include those associated with the central nervous system including psychiatric or neurological disorders, especially ischemmia-related conditions such as strokes, and also includes neurodegenerative disorders such as Alzheimer's disease, Huntington's disease, The modulators may also be 

Vascular diseases such as ischemmic encephalopathy or cerebral infarction; eye conditions such as diabetic retinopathy or macular degeneration; eye conditions such as diabetic retinopathy or macular degeneration; hypertension; myocardal infarction; atherosclerosis; respiratory conditions such as sathma or chronic obstructive pulmonary disease; neoplastic conditions such as cancers or benign tumours; blood cell conditions such as anaemia; gastrointestinal conditions such as gastritis or ulcerative colitis; liver conditions such as biliary cirrhosis; kidney disorders such as glomerulonephritis; cystitis; endocrine disorders such as drawe's disease or Hashimoto's hyproiditis; skin conditions such as dermatitis or unticaria; or immune system disorders such as acquired immunodeficiency syndrome (AIDS). The nucleic acids may additionally be used to generate animal models of cell death-protective polypeptide. ö Gaps Gene 41 human secreted protein homologous amino acid sequence #157. ö Length 363; 100.0%; Score 37; DB 22; Length 3 100.0%; Pred. No. 2.6; ive 0; Mismatches 0; Indels AAB45216 standard; Protein; 403 AA. Query Match Best Local Similarity 100... 8; Conservative 12-FEB-2001 (first entry) 107 LYQAVATI 114 1 LYQAVATI 8 363 AA; AAB45216; RESULT 5 AAB45216 δλ Dp 

Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungloide; cancer; opthalmalogical; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; septom disorder; aging; chemotaxis.

Homo sapiens.

WO200058467-A1.

05-OCT-2000.

22-MAR-2000; 2000WO-US07505.

99US-0126502. 26-MAR-1999;

99US-0172410. 17-DEC-1999; (HUMA-) HUMAN GENOME SCI INC

Komatsoulis G; Rosen CA, Ruben SM,

WPI; 2000-611712/58.

Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -

Disclosure; Page 60-61; 440pp; English.

Polynucleotide sequences AAC80531-C80580 represent cDNA encoding human secreted proteins AAB45120-B45169. Sequences AAB45170-B45255 represent alternative polypeptides encoded by the genes, and amino acid sequences to which they are homologous. The genes and proteins have activities dependent on the tissues and cells in which they are expressed. Examples of their activities include immunosuppressive; antiarthritic;

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cerebroprotective; nontropic; neuroprotective; antibacterial; virucide; and opthalmalogical. The secreted proteins, polynucleotides, antagonists and agonists may be useful in treating, preventing and/or antagonists and agonists may be useful in treating, preventing and/or diagnosing diseases and disorders such as autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral isohemia, anglogenesis, nervous system disorders e.g. Alzheiner's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin adjudent oclusions, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotraxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAC80822-C80530 and ABA4519 represent sequences used in the isolation and characterisation of the genes and proteins of
   antirheumatic; antiproliferative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the invention.
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403 AA; Sequence

0; 100.0%; Score 37; DB 21; Length 403; 100.0%; Pred. No. 3; 0; Indels 0; Mismatches Ouery Match Best Local Similarity الهن. احد 8; Conservative

||||||||| 154 LYQAVATI 161 1 LYQAVATI 8 g ŏ

RESULT 6 AAB45217

AAB45217 standard; Protein; 404 AA.

AAB45217;

12-FEB-2001 (first entry)

Human secreted protein sequence encoded by gene 41 SEQ ID NO:158.

Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; noncropic; neuroprotective; antibacterial; virucide; funglicide; cancer; opthalmalogical; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; serebrovascular disorder; aging; chemotaxis. 

Homo sapiens.

WO200058467-A1

05-OCT-2000

22-MAR-2000; 2000WO-US07505.

99US-0126502. 99US-0172410. 26-MAR-1999; 17-DEC-1999; (HUMA-) HUMAN GENOME SCI INC

Komatsoulis G; Ruben SM, Rosen CA,

WPI; 2000-611712/58. N-PSDB; AAC80571

Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's Parkinson's diseases and cancers -

Disclosure; Page 60-61; 440pp; English.

Polynucleotide sequences AAC80531-C80580 represent cDNA encoding human secreted proteins AAB45120-B45169. Sequences AAB45170-B4525 represent

e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, andiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburr, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAC80522-C80530 and AAB45119 represent sequences used in the isolation and characterisation of the genes and proteins of the invention. alternative polypeptides encoded by the genes, and amino acid sequences to which they are homologous. The genes and proteins have activities dependent on the tissues and cells in which they are expressed. Examples of their activities include immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; noctropic; neuroprotective; antibacterial; virucide; fungicide; and opthalmalogical. The secreted proteins, polynucleotides, antagonists and agonists may be useful in treating, preventing and/or diagnosing diseases and disorders such as autoimmune diseases

404 AA; Sequence

Gaps ö 100.0%; Score 37; DB 21; Length 404; 100.0%; Pred. No. 3; ive 0; Mismatches 0; Indels 0 Ouery Match Best Local Similarity 100..

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δy

AAG98644

AAG98644 standard; Protein; 412 AA.

21-SEP-2001 (first entry)

Human cell death protective cDNA clone CNI-00714 ORF1 protein, SEQ:77.

Cell death protective; apoptosis; necrosis; human; drug screening; cell death-associated disorder; central nervous system disorder; psychiatric disorder; neurological disorder; ischaemia-related disorder; stroke; cerebral infarction; ischaemic encephalopathy; neurodegenerative disorder; Alzheimer's disease; Huntington's disease; Parkinson's disease; infection; meningitis; malaria; trypanosomiasis; wascular disease; opthalmological disorder; diabetic retinopathy; anacular degeneration; hypertension; myocardial infarction; atherosclerosis; respiratory disorder; asthma; transgenic animal; chronic obstructive pulmonary disease; neoplastic condition; cancer; benign tumour; anaemia; gastrointestinal disorder; gastriitis; uloerative colitis; liver disease; biliary cirrhosis; kidney disorder; glomerulonephritis; cystitis; endometriosis; endometricis; e Grave's disease; Hashimoto's thyroiditis; skin condition; dermatitis; urticaria; immune disorder; acquired immunodeficiency syndrome; AIDS.

Homo sapiens.

WO200145638-A2

28-JUN-2001.

11-DEC-2000; 2000WO-US33547.

99US-0461697. 14-DEC-1999; (COGE-) COGENT NEUROSCIENCE INC.

Katz LC; Puranam K, Barney S, Thomas MB, Portbury SD, Lo DC,

98JP-0341253. 99WO-JP06682.

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Included in the invention are polynucleotide sequences encoding the ART-1 protein, and mutated ART-1 proteins which when broken down intracellularly produce a tumour antigen peptide that can recognise HIA antigen and bound cyrotoxic T cells. Antibodies which specifically recognise ART-1 and its derivative peptides, are also included in the protein, tumour antigen peptide originating from it, their derivatives, and DNAs are applicable in vivo or in vitro as remedies, preventives and
                                                                                                                                                                                                                                                                                                                                           Novel tumor antigen protein ART-1, tumor antigen peptide originating from it, their derivatives, and DNAs, applicable in vivo or in vitro as remedies, preventives and diagnostics for tumors \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel human tumour antigen protein, ART-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents the human ART-1 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 44-46; 59pp; Japanese.
                                                                                                                                                             SUMU ) SUMITOMO PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnostics for tumours.
                                                                                                                                                                                                                                                                           WPI; 2000-412318/35.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 414 AA;
                                                                                                                                                                                                                                                                                                N-PSDB; AAA62864.
                                                                                                                                                                                  ITOH/) ITOH K.
                                                                  30-NOV-1999;
                                                                                                                01-DEC-1998;
                       08-JUN-2000.
                                                                                                                                                                                                                             Itoh K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                    CC Protect against cell death (i.e., apoptosis or necrosis). Sequences which protect against cell death (i.e., apoptosis or necrosis). Sequences which protect against cell death (i.e., apoptosis or necrosis). Sequences which protect against cell death (i.e., apoptosis or necrosis). Sequences while the remaining nucleic acid sequences within the range given above represent the open reading frames (ORFs) of these CDMA clones. Sequences AAG98610-AAG98829 represent the polypetides encoded by the cell death protective onk clones are able to protective ORFs. The cell death protective cDNA clones are able to protective ORFs. The cell death protective onk clones are able to protective ORFs. The cell death protective onk clones are able to protective ORFs. The cell death protective onk clones are able to protective ORFs. The cell death protective onk clones are able to protective ORFs. The cell death protective onk clones are able to protective ORFs. The cell death protective or cell predisposed to or undergoing cell death, and to screen for compounds which modulate their activity or expression. Such modulators, preferably a small organic molecule, an antibody. The diagnosis and treatment of disorders associated with cell death, and to screen for compounds which modulate those associated with the cell death aribaced diseases. Such diseases include those associated with the central nervous system including psychiatric or neurological cell death-related disorders such disorders such as Alzheimer's disease, and also includes neurodegenerative disorders such as Alzheimer's disease, and class includes neurodegenerative disorders such as meningitis, malaria, or trypanosomiasis; cused to treat infections such as meningitis, malaria, or trypanosomiasis; cused to treat infections such as atlandaria certifications such as antenia gastrointestinal conditions such as anemia gastrointestinal calds may addi
                                                                                                                                                                                                                           Sequences AAH84132-AAH84370 represent human nucleic acid sequences which
                                                                                   Novel protective sequence polynucleotides and polypeptides, used to identify modulators of their expression and activity, which are used in to treat central nervous system conditions, diseases and disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell death protective polypeptide.
                                                                                                                                                                              Claim 1; Fig. 6A; 325pp; English.
                                        N-PSDB; AAH84170, AAH84171.
                   2001-390297/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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Gaps

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0; Indels

100.0%; Score 37; DB 21; 100.0%; Pred. No. 3.1; Live 0; Mismatches 0;

8; Conservative

158 LYQAVATI 165

1 LYQAVATI 8

Length 414;

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Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
                                                                                                              Human protein sequence SEQ ID NO:1360.
 AAM25845 standard; Protein; 419 AA.
                                                                          16-OCT-2001 (first entry)
                                      AAM25845;
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                                                                            Gaps
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                                  100.0%; Score 37; DB 22; Length 412; 100.0%; Pred. No. 3;
                                                                      0; Indels
                                                                        Mismatches
                                                                                                                                                                                                                                        AAB03880 standard; protein; 414 AA.
                                                                        0;
                                                                                                                                                                                                                                                                                                                                                  Human ART-1 protein sequence.
                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                        8; Conservative
                                                                                                                                              156 LYQAVATI 163
                                                                                                          1 LYQAVATI 8
                                                     Best Local Similarity
412 AA;
                                                                                                                                                                                                                                                                                                                26-OCT-2000
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Matches

RESULT 8 AAB03880

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antinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; antibacterial; endocrine; cardiovascular; antianaemic; anaemia; antiagregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antialergic; antiasthmatic; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
                                                                                                                                                                                                                                                                                                                                                             antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoletic disorder; platelet disorder; astuma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurological disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200153455-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
Human; tumour antigen protein; ART-1; HLA antigen; cytostatic; bound cytotoxic T cell; tumour; cancer; remedy; prevent; diagnose.
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WO200032770-A1 Homo sapiens.

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Streptococcus/GBS (Streptococcus/GBS) to a properties or group A streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS) comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antihilammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used to recombosition. The disease caused by Streptococcus that is prevented or treated may be maningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                               New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cenarchaeum symbiosum open reading frame protein sequence SEQ ID NO:56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a protein (ABP25413-ABP30895) from group B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cenarchaeum symbiosum; non-thermophilic; crenarchaeote; physiology; characterisation; archae; therapeutic; industrial; laboratory.
                                                                                                                                                                                                                                      Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.5%; Score 32; DB 23; Length 100; 87.5%; Pred. No. 8.8; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                      Grandi G,
                                                                                                                                                                                                                                      Telford J, Masignani V, Margarit Ros YI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 3807; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY90939 standard; Protein; 273 AA.
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                                                                 27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                    29-OCT-2001; 2001WO-GB04789.
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Matches 7; Conservative
                                                                                                                                                                                           (GENO-) INST GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus proteins
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                                                                                                                                                                                                                                                                                                             WPI; 2002-352536/38.
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                                                                                                                                                                  (CHIR-) CHIRON SPA
                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABN69268
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                                                                                                                                                                                                                                                                  rettelin H;
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q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthruttis they are expressed in, such as: antiinflammatory; antirheumatic; cells they are expressive; antibacterial; endocrine; cardiant; cardiancesive; antibacterial; endocrine; cardiant; cardiancesive; antiagregant; hemeostatic; unloreray; antiparkinsonia; and immunostimulant. The proteins and polynucleotides antiparkinsonian; and immunostimulant. The proteins and polynucleotides antiparkinsonian; and immunostimulant. The proteins and polynucleotides concoding them can be used in gene therapy, antisense therapy and vaccine production, The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation; heumatold arthritis, septic shock, pancteatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, hemmatopoictic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, chinitis, asthma, disease, thrombocytopaenia, wounds, burns, ulcers, chinitis, asthma, disease, parkinson's disease, neurodegenerative and chinitis, and disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                               Isolated human polynucleotides encoding polypeptides, useful for treatment and diagnosis of e.g. cancer, ulcers and HIV infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 37; DB 22; Length 419; 100.0%; Pred. No. 3.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; Page 281; 1217pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP28637 standard; Protein; 100 AA.
                                                                                                                                                                                                                                                          Pang YT, Liu C, Drmanac RT;
                                                                                                            23-DEC-1999; 99US-0471275.
21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
                                                                 22-DEC-2000; 2000WO-US35017
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pyogenes
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                                                                                                                                                                                                                                                                                                             WPI; 2001-457603/49.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                419 AA;
                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAH99786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200234771-A2.
                    26-JUL-2001.
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RESULT 10 ABP28637

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Gaps

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Gaps

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Length 269;

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AAY45390 to AAY48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA) binding motif. The immunogenic peptides can bind to a specific HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived. Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are perticularly important in tumnour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, ALDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenic peptide having a human leukocyte antigen binding motif #2505
and proteins isolated from the non-thermophilic crenarchaeote Cenarchaeum symbiosum. The nucleic acids and proteins identified in the present invention are useful in characterising the physiology of these archae and can be used in therapeutic, industrial or laboratory techniques. AAA5527 to AAA55260 represent promoter sequences from Cenarchaeum symbiosum. AAA55261 to AAA55269 represent PCR primers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         motif, useful in treatment
                                                                                                                                                                                                          1; Indels
                                                                                                       probes used in examples from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grey HM,
                                                                                                                                                                         21;
                                                                                                                                                                    DB
47;
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                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Celis E,
                                                                                                                                                                         Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 126; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                          AAY47894 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sidney J,
                                                                                                                                                                       83.8%;
75.0%;
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                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; immunisation
                                                                                                                                                                                                                                                                         174 LYQAVPTV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EPIM-) EPIMMUNE INC.
                                                                                                                                                                                                                                        1 LYQAVATI 8
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                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                        269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                             AAY47894;
                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                          AAY47894
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                                                                                                                                 New nucleic acids and proteins isolated from the non-thermophilic crenarchaeote Cenarchaeum symbiosum, useful in characterizing the physiology of these archae and in therapeutic, industrial or laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         crenarchaeote Cenarchaeum symbiosum, useful in characterizing the physiology of these archae and in therapeutic, industrial or laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cenarchaeum symbiosum open reading frame protein sequence SEQ ID NO:24
                                                                                                                                                                                                                                                                                                  the present invention are useful in characterising the physiology of these archae and can be used in therapeutic, industrial or laboratory techniques. AAA55277 to AAA55260 represent promoter sequences from Cenarchaeum symbiosum. AAA55261 to AAA55269 represent PCR primers and probes used in examples from the present invention.
                                                                                                                                                                                                                                                          nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                   AAA55186 to AAA55226 and AAY90913 to AAY90951 represent nucleic acid and proteins isolated from the non-thermophilic crenarchaeote Cenarchaeum symbiosum. The nucleic acids and proteins identified in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cenarchaeum symbiosum; non-thermophilic; crenarchaeote; physiology; characterisation; archae; therapeutic; industrial; laboratory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acids and proteins isolated from the non-thermophilic
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32; DB 21; Length 273;
Pred. No. 28;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                  Schleper C;
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                                                                                                                                                                                                                   Claim 26; Page 171; 210pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY90923 standard; Protein; 269 AA.
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87.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 87.5.
7; Conservative
                                                Feldman RA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cenarchaeum symbiosum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYQAVPTI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cenarchaeum symbiosum
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                 (DIVE-) DIVERSA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DIVE-) DIVERSA CORP.
                                                                                2000-293148/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LYQAVATI 8
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                                                                                                                                                                                                                                                                                                                                                                                                       273 AA;
                                                                                                   N-PSDB; AAA55214
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                                                  Swanson RV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-AUG-2000
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                                                                                                                                                                                    techniques
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Vaccine for immunizing against human immunodeficiency virus has mixture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or linear array of peptides comprising immunodominant T-helper epitopes and major histocompatibility complex cytotoxic T-lymphocyte epitopes
                                                                                                                                                       Human immunodeficiency virus, HIV; immunogen; vaccine; anti-HIV; human leukocyte antigen; HLA; T-helper epitope; CTL; Th; epitope; major histocompatibility complex; MHC; cytotoxic T-lymphocyte;
                                                                                                                       Human HIV-1 Th-CTL overlapping epitope #48.
                                                                                                                                                                                                                                             Homo sapiens.
Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 27; 33pp; English.
                   AAU12541 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                   05-FEB-2001; 2001WO-US03540
                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000; 2000US-0497497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haynes BF, Liao H;
                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYDU-) UNIV DUKE.
                                                                                                                                                                                                             Vaccinia ankara.
                                                                                                                                                                                                                                                                                                 WO200156355-A2.
                                                                                       27-SEP-2001
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                                                     AAU12541;
     AAU12541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to identification of cytotoxic T cell lymphocyte (CTL) epitopes (AAM22116-AAM23484) that generate anti-HIV activity. CTL are a major protective mechanism against viral diseases. Antibodies may neutralise extracellular human immunodeficiency virus (HIV) and limit or prevent infection of cells in the host, but CTL will limit viral production by killing the cell. The CTL epitopes are useful in medicine, in the manufacture of vaccines or diagnostic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hansen J;
                                                                                                                                                                           Gaps
useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The polynuclectides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTL; anti-HIV; viral disease; HIV;
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                                                                                                                                         Length 9;
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                                                                                                                                                                           1; Indels
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                                                                                                                                       Score 30; DB 20;
Pred. No. 7.8e+05;
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                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human immunodeficiency virus; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 13; Page 53; 383pp; English.
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                                                                                                                                                                                                                                                                                                                                 AAM22249 standard; Peptide; 9 AA
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                                                                                                                                         81.1%;
75.0%;
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31-JAN-2000; 2000US-0179333
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                                                                                                                                                                                                                                                                                                                                                                                                                                   HIV peptide SEQ ID NO 134.
                                                                                                                                                                           6; Conservative
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                                                                                                                                                                                                                             WPI; 2001-476184/51.
                                                                                                                                     Query Match
Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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                                                                                                       9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytotoxic T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                   AAM22249;
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The present invention relates to human immunodeficiency virus (HIV) and in particular to a human leukocyte antigen (HLA)-based HIV vaccine. The vaccine comparises a mixture or linear array of peptides, or its variants, where the peptides contain immunodominant T-helper (Th) epitopes and major histocompatibility complex (MHC) cytotoxic T-lymphocyte (CTL) epitopes and the linear array of peptides are preferably expressed in modified Vaccinia ankara. The vaccine is useful for immunising a patient against HIV and focuses immune response on many dominant and subdominant CTL epitopes of HIV. DNA or live vectors with
                                                                                                                                                                                                                                                                                                                          linear arrays of CTL epitopes can be used as either primes or boosts of peptides or of each other to optimally give CTL anti-HIV responses. The vaccine induces salutary anti-HIV immune responses. AAU12447-AAU12558 represent the amino acid sequences of the Th-CTL epitopes and HIV immunogenic peptides used in the invention.
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Pred. No. 7.8e+05;
1; Mismatches 1
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75.08;
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Best Local Similarity 75.0
Matches 6; Conservative
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Conservative

1 LYQAVATI 8 

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RESULT 15

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EMBL; AB018307; BAA34484.1; -.
EMBL; AF197954; AAG28523.1; -.
SEQUENCE 414 AA; 46192 MW; 59724A96353D44D5 CRC64;
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                                                                                                                                                                                                                                                            Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A alto T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Sakai K., Okido T., Futulo T., Gissi C., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Futuno M., Aono H., Baldarelli R., Barsh G.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Whittaker C., Whittaker C., Willining L.,
A Whinshaw Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Whasehisahi V.
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                                                     Mus musculus (Mouse).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mos
NCBI_TaxID=10090;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MGD; MGI:1919445; 2610524B01Rik.
SEQUENCE 412 AA; 45970 MW; B7BF1525BB44F6D5 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
KIAA0764 protein (Adenocarcinoma antigen ARTI).
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STRAIN-C57BL/6J; TISSUE-EMBRYO;
MEDLINE-21085660; Pubmed-11217851;
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SEQUENCE FROM N.A.
MEDLINE-20441578; Pubmed-10987294;
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nes 8; Conservative
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2610524B01Rik protein. 2610524B01RIK.
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Development 121:3335-3346(1995).
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"The CHESS Protein domain: a novel structural unit that is common among networks involved in cell signaling, chromatin metabolism and cell division.";
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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SEQUENCE 891 AA; 101976 MW; 394A12B904D06899 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
BUB2-like protein I (Vascular RAB-GAP/TBC-containing).
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MEDLINE-96017645; PubMed-7588067;
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InterPro; IPR004182; GRAM_dom.
InterPro; IPR000195; RabGAP_TBC.
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TISSUE-HEMATOPOIETIC;
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SEQUENCE FROM N.A.
TISSUE=ADENCCARCINOMA;
MEDLINE=20441578; PubMed=10987294;
Nishizaka S., Gomi S., Harada K., Oizumi K., Itoh K., Shichijo S.;
"A new tumor-rejection antigen recognized by cytotoxic T lymphocytes
infiltrating into a lung adenocarcinoma.";
Cancer Res. 60:4830-4837(2000).
EMBL; AF224759; AAG47636.1; -.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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|156 LYQAVATI 163
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074043 cenarchaeum
0811s0 methacum
081081 schizosacch
07466 cenarchaeum
036923 human immun
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MEDLINE=98422450; PubMed=9748430; Schleper C., DeLong E.F., Preston C.M., Feldman R.A., Wu K.Y., Schleper C., DeLong E.F., Preston C.M., Feldman R.A., Wu K.Y., Swanson R.V.; Genomic analysis reveals chromosomal variation in natural populations of the uncultured psychrophilic archaeon Cenarchaeum symbiosum."; J. Bacteriol. 180:5003-5009(1998).
EMBL; ARG28071; ARG2686.1; -. InterPro; IPR003115; ParBc.
                                                                                                                                                                                     Pfam; PF02195; ParBc; 1.
SMART; SM00470; ParBc; 1.
TIGRFAMS; TIGR0180; ParB_part; 1.
Hypochetical protein: SEQUENCE 273 AA; 31103 MW; 683C683F18DF61BE CRC64;
  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                         86.5%; Score 32;
87.5%; Pred. No.
           Hypothetical 31.1 kDa protein.
Cenarchaeum symbiosum.
Archaea; Crenarchaeota; Cenarchaeum.
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                          178 LYQAVPTI 185
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                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                          NCBI_TaxID=46770;
                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                     1 LYQAVATI
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MEDLINE=99303817; PubMed=10373574;
Wonekura H., Migita H., Sakurai S., Wang H., Harada S., Abedin M.J.,
Yamaqishi S., Yamamoto H.;
"Antisense display-a method for functional gene screening: evaluation
in a cell-free system and isolation of angiogenesis-related genes.";
Nucleic Acids Res. 27:2591-2600(1999).
EMBL: AB024057; BAA7548911; ...
InterPro: IPR00195; GRAM_dom.
InterPro: IPR00195; RabGAP_TBC.
Pfam: PF02583; GRAM_i. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales; Streptococcaceae; Streptococcus. NCBL_TaxID=1314;
                            Eukaryora, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 18;
                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                           SMART; SM00164; TBC; 1.
SEQUENCE 897 AA; 102676 MW; D498C280A657BD1C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical protein SPy0914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O74043 PRELIMINARY; PRT; 273 AA. 074043; 01-NOV-1998 (TrEMBLrel. 08, Created) 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
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Pred. No. 8.5;
0; Mismatches 1;
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Vascular Rab-GAP/TBC-containing protein.
                                                                                                                                                                                                                                                                                                                                                                      PRT;
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Best Local Similarity 87.5%;
Matches 7; Conservative
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                Query Match
Best Local Similarity
6; Conserve
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                                                  NCBI_TaxID=9606;
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074043
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Gaps

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Length 273;

DB 26;

0; Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The genome of Methanosarcina acetivorans reveals extensive metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                            Archaea; Euryarchaeota; Methanococci; Methanosarcinales; Methanosarcinaceae; Methanosarcina.
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                                                          01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
485 AA
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1; Mismatches
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MEDLINE=21929760; PubMed=11932238;
PRT;
                                                                                                                                                               Proton/sodium-glutamate symporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and physiological diversity.";
Genome Res. 12:532-542(2002).
EMBL; AEO10998; AAMO6334.1; -
Complete proteome.
                                                                                                                                                                                                                                 Methanosarcina acetivorans
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Best Local Similarity 75.0
Matches 6; Conservative
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RESULT 9

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STRAIN-LN23;

MEDLINE—99412391; PubMed=10482626;

MEDLINE—99412391; PubMed=10482626;

MOTIS A., Marsden M., Halcrow K., Hughes E.S., Brettle R.P.,

Morais A., Marsden M., Halcrow K., Hughes E.S., Brettle R.P.,

"Mosaic structure of the human immunodeficiency virus type 1 genome
infecting lymphoid cells and the brain: evidence for frequent In vivo

"Infecting lymphoid cells and the brain: evidence for frequent In vivo

"Infecting lymphoid cells and the evolution of regional populations.";

J. Virol. 73:8720-8731(1999).

BEBL; AFIA940; AFEGO386.1; -.

REBL; AFIA940; AFEGO386.1; -.

REPLY PRO0244; HIVIMATRIX.

RAIDS; Core protein; Polyprotein.

THON TER 129 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The molecular epidemiology of human immunodeficiency virus type 1 in six cities in Britain and Ireland.";
Virology 235.166-177(1997).
EMBL; AF014320, AAC58401.1; -.
Interbro; IPR000071; Retrovir_p17.
Pfam; PF00540; Gag_p17; 1.
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97445059; Pubmed-9300048; Leigh Brown A.J., Lobidel D., Wade C.M., Rebus S., Phillips N., Brettle R.P., France A.J., Leen C.S., McMenamin J., McMillan A., Phan R.D., Mulcahy F., Robertson J.R., Sankar K.N., Scott G., Wyld R., Peutherer J.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 129;
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                                                                                                                                                                                01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
GAG polyprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                             PRELIMINARY;
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                           ||||| |:
174 LYQAVPTV 181
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    1 LYQAVATI
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NON_TER
SEQUENCE
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EMBL: AF083072; AAC62709.1; ...
InterPro: IPR003115; ParBc.
InterPro: IPR004437; ParBc.
InterPro: IPR004437; ParBc.
SMART: SM0470; ParBc: 1.
Fign: PF02195; ParBc: 1.
FIGRFAMS; IRG00180; ParBc: 1.
Hypothetical protein.
SEQUENCE 269 AA; 30689 MW; AA45216CAD16DD5B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                              STRAIN=972H-;
Wedler H., Duesterhoeft A., McDougall R.C., Rajandream M.A.,
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32; DB 3; Length 865; Pred. No. 92; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AL117183; CAB54865.1; ... InterPro; IPR002553; Adaptin_N. InterPro; IPR001121; Gamma_adaptin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam: PF01602; Adaptin_N; 1. Pfam: PF02883; Alpha_adaptinC2; 1. ProDom: PD021457; Gamma_adaptin_C; 1. SEQUENCE 865 AA; 96041 WW; 05BA43A15B61E84E CRC64;
                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 30.7 kDa protein.
Cenarchaeum symbiosum.
Archaea: Createdaeota; Cenarchaeum.
NCBI_TaxID=46770;
                                                                                                                                                              Last sequence update)
Last annotation update)
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                                                                                                                                             Created)
                                                                                                     PRT;
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Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21,
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                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                   Putative gamma-adaptin.
SPCP1E11.06.
348 LYQGVATV 355
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                                                                                                                                                                                                                                                                                                     Schizosaccharomyces.
NCBI_TaxID=4896;
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Best Local Similarity
Matches 6; Conserv
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Q90081;
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Gaps

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Length 129

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129 129
129 AA; 14474 MW; 007EF7119CFFEF41 CRC64;
                                                                                                                                                                                                 81.1%; Score 30; 75.0%; Pred. No.
  EMBL; AF174947; AAF00293.1; -.
InterPro; PR000071; Retrovir_p17.
Pfam; PF00540; Gag_p17; 1.
PRINTS; PR00234; HIVIMATRIX.
                                                                                        AIDS; Core protein; Polyprotein.
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55 LYNAVATL 62
                                                                                                                                                                                                                                                                                     1 LYQAVATI 8
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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SEQUENCE
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J. Virol. 73:8720-8731(1999).
EMBL: AF174941; AAF00287.1;
InterPro: IPR000071; Retrovir_p17.
Pfam: PF00540; Gag_p17; 1.
PRINTS; PR00234; HIVIMATRIX.
ANDS: Core protein; Polyprotein.
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MORFIS A., Marsden M., Halcrow K., Hughes E.S., Brettle R.P.,
Bell J.E., Simmonds P.;
                                             Length 129;
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129 AA; 14574 MW; C24B7A48456E2EE0 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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MEDLINE=97445059; PubMed=9300048;
Leigh Brown A.J., Lobidel D., Wade C.M., Rebus S., Phillips N.,
Brettle Brown A.J., Leen C.S., McMenamin J., McMillan A.,
Brettle R.P., France A.J., Leen C.S., McMenamin J., McMillan A.,
Maw R.D., Mulcahy F., Robertson J.R., Sankar K.N., Scott G., Wyld R.,
Peutherer J.F.;
The molecular epidemiology of human immunodeficiency virus type 1 in
six cities in Britain and Ireland.";
Virology 235:166-177(1997).
EMBL, AF014229, AACSB310.1; -.
EMBL, PR014229, AACSB310.1; -.
EMBL, PR014209, Gag_pl7; 1.
PERNTS; PR00234; HIVIMATRIX.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
DB 15;
34;
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July 18, 2003, 09:46:58; Search time 90.2559 Seconds (without alignments) 945.129 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp\_fungi:\*
sp\_human:\*
sp\_invertebrate:\*

sp\_mammal:\*

7: sp\_mhc:\*

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SPTREMBL\_21:\*

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sp\_organelle:\* sp\_phage:\* 15: sp\_rvirus:\*
16: sp\_bacteriap:\*
17: sp\_archeap:\*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_unclassified:\*

sp\_vertebrate:\*

sp\_plant:\*
sp\_rodent:\*
sp\_virus:\*

Sa	Description	094864 homo sapien	09h2t6 homo sapien	Q9czv5 mus musculu	P87152 schizosacch	09vx12 drosophila	09vi49 drosophila	09kta5 vibrio chol	08x0v8 neurospora	O61845 caenorhabdi	O9vap9 drosophila	099pis mus musculu	O9er99 mus musculu	09v4v2 homo sapien	096hv9 homo sapien	09zlp7 mus musculu	Curedmecore Carro
SUMMARIES	ID	094864	Q9H2T6	Q9CZV5	P87152	09VX12	09VI49	Q9KTA5	08X0V8	061845	Q9VAP9	Q99PI5	Q9ER99	Q9Y4V2	6АН960	09Z1P7	CMVZPO
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17 114 5.2 486 11 Q90X18 18 113 5.2 1152 4 Q92603 20 113 5.2 1204 4 Q91G2 21 112 5.1 1852 5 Q9VH42 22 112 5.1 486 4 Q9UNFO 23 111.5 5.1 1278 4 Q9UNFO 24 111.5 5.1 1278 3 Q8X0X7 26 109.5 5.0 16215 5 Q9YIG8 27 109.5 5.0 16215 5 Q9YIG8 28 109 5.0 66215 5 Q9YIG8 29 109 5.0 67215 5 Q9YIG8 30 108.5 5.0 1206 11 Q9WVE8 31 108.5 5.0 1206 11 Q9WIG8 32 108.5 5.0 1206 12 Q9DIG8 33 108.5 5.0 1266 5 Q9YIG8 34 107.5 4.9 568 12 Q9DIG2 35 107.5 4.9 568 12 Q9DIG3 36 107 4.9 884 5 Q9YEV9 37 107 4.9 884 5 Q9YEV9 38 107 4.9 268 5 Q9YIG8 39 107 4.9 268 5 Q9YIG8 30 107 4.9 268 5 Q9YIG8 31 107 4.9 268 5 Q9YIG8 32 107 4.9 268 5 Q9YIG8 33 107 4.9 268 5 Q9YIG8 34 107 6 4.9 599 10 Q9ZIG5 41 106 4.9 599 10 Q9ZIG5 42 106 4.9 667 5 Q9YIG9 43 106 4.9 667 5 Q9YIG9		Q91rr7 arabidopsis O16938 caenorhabdi O18673 caenorhabdi Q9tvi9 caenorhabdi Q17490 caenorhabdi
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## ALIGNMENTS

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Nagase T., Ishikwa K., Suyama M., Kikuno R., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;

**Rediction of the coding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";

**PDNA Res. 5:277-286(1998).
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MEDLINE-20441578; PubMed=10987294;
Nishlazaka S., Gomla. S., Harada K., Olzumi K., Itoh K., Shichijo S.;
Nishlazaka S., Gomla. S., Harada K., Olzumi K., Itoh K., Shichijo S.;
infiltrating into a lung adenocarcinoma.";
Cancer Res. 60.4830-4837(2000).
EMBL; AB018307; BAA34484.1; -.
EMBL; AB018307; BAA34484.1; -.
SEQUENCE 414 AA; 46192 MW; 59724A96353D44D5 CRC64;
                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                         01-MX-1999 (TrEMBLrel. 10, Created)
01-MX-1999 (TrEMBLrel. 10, Last sequence update)
01-MXR-2001 (TrEMBLrel. 16, Last annotation update)
KIAA0764 protein (Adenocarcinoma antigen ART1).
KIAA0764.
                                     414 AA.
                                     PRT;
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MEDLINE=99087487; PubMed=9872452;
                                     PRELIMINARY;
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SEQUENCE FROM N.A.
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RESULT 1
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1 MNLQRYWGEIPISSSQTNRSSFDLLPREFRLVEVHDPPLHQPSANKPKPPTMLDIPSEPC

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Db 243 YMLQISKQLSEEYERIVNPEKATEDAKPVKIKEEPVSDITFPVSEELEADLASGDQSLPM 302  Qy 305 GVLGAQSERFPSNLEVEASPQASSAEVNASPLWNLAHVKMEPQESEEGNVSGHGVLGSDV 364	RESULT 3 Q9CZV5 ID Q9CZV5 O9CZV5 AC Q9CZV5; DT 01-JUN-2001 (TrEMBLrel. 17, Created) DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) DE 2610524B01R1k protein. CN Mus musculus (Mouse). OC Mus musculus (Mouse). OC Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Buteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. NO NCBL_TaxID=10090;	RP SEQUENCE FROM N.A.  RP STANN=C5PLE/65; TISSUE=EWBRYO;  RX MEDLINE=21085660; PubMed=11217851;  RA ARAWAWA T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  RA Arawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  RA Arawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  RA Aizawa K., Isawa M., Nishi K., Kiyosawa H., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Yamanaka I.,  RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  RA Kedota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  RA Ivons P. Marchioni I. Mashima M., Kanaka M., Kamiya M., Lee N.H.,	RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch KF., RA Suzuki H., Toyo-oka K., Mang K., Hasegawa Y., Shibata Y., Storch KF., RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., RA Haysshizaki Y.; RA Haysshizaki Y.; RI "Functional annotation of a full-length mouse cDNA collection."; RL Nature 409:685-690(2001). DR EMBL; AK012134: BAB28053.1; DR MGD; MGI:1919445; 2610524BNIRK. SQ SEQUENCE 412 AA, 45970 MW; B7BF1525BB44F6D5 CRC64; Ouery Match Best Local Similarity 95.9%; Pred No. 9.2e-159;	SIMILATITY 95.9%; Pred. 3; Conservative 7; Mistrage 7; Mistrage 11; Millill 11 11 11 11 11 11 11 11 11 11 11 11 1
	181 TLTDVAHEYCLKFTKLLRFAVDREARLGQTPEPDVMEQVFHEVGIGSVLSLQKFWQHRIK 240	361 GSDVFEEPMSGMSEAGIPQSPDDSDSSYGSHSTDSLMGSSPVFNQRCKKRMRKI 414		63 HTIQLIQHNRRLRNLIATAQAONQQTEGVKTEESEPLPSCPGSPPLPDDLLPLDCKNPN 122- 125 APFQIRHSDPESDFYRGKGEPVTELSWHSCRQLLYQAVATILAHAGFDCANESVLETLTD 184

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351 EGNVSGHGVLGSDVF-----EEPMSGMSEAGIPQSPDDSDSSYGSHSTDSLMGSSPVF 403
                        Last annotation update)
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FlyBase; FBgn0030874; CG6506.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EADLASGDQSLPMGVLGAQSERFPSNLEVEASPQAS-SAEVNASPLWNLAHVKMEPQESE 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   844 DRELGLDSLSVPLHLL---OSRLRSNMSWQ--PEATIKGDQEYAPPFKYPPITAESISNE 898
                                        GVLGAQSERFPSNLEVEASPQASSAEVNASPLWNLAHVKMEPQESEEGNVSGHGVLGSDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 IPISSSQT--NRSSFDLLPREFRLVEVHDPPLHQPSANKPKPPTMLDIPSEPCSLTIHTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          784 VKLLEIHQRLQRHFVELLRPALSERNDEEAIFNONGESFVTGNFSYETGDDFFGLRELGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         596 VPMTAGSVLETESEEDLYFRDYSLFEI------NRNTPGVP-----SLMYKNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00633; BROMODOMAIN 1; 1.
PROSITE; PS50014; BROMODOMAIN 2; 1.
Hypothetical protein; Transcription regulation; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87;
                                                                                365 FEEPMSGMSEAGIPQSPDDSDSSYGSHSTDSLMGSSPVFNQRCKKRMRKI 414
                                                                                                                                                                                                                                                                                                   Church C., Wood V., Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYMLQISKQLSEEYERIVNPEKATEDAKPVKIKEEPVSDITFPVSEE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.6%; Score 142.5; DB 3; Length 9
19.4%; Pred. No. 0.011;
Ive 74; Mismatches 183; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               BROMODOMAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Last annotation u
Putative transcriptional activator C25H2.11C.
                                                                                                                                            979 AA.
                                                                                                                                                                                                      SPBC25H2.11C.
Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                     P87152;
01-JUN-1998 (TrEMBLrel. 06, Created)
                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                     InterPro: IPR011487; Bromodomain.
Pfam; PF00439; bromodomain; 1.
SMART; SM00297; BROMO; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Activator; Bromodomain.
                                                                                                                                                                                                                                               Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       979 AA;
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                          01-JUN-1998
                                                                                                                                                                                                                                                                                         STRAIN-972;
                              305
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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RAIN MEDELINE—20196006; PubMed=10731132;

RAIN MEDELINE—20196006; PubMed=10731132;

RAIN MEDELINE—20196006; PubMed=10731132;

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Brandon R.C., Mortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Brandon R.C., Barster E.G., Helf G. Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,

Ballew R.M., Benos P.V., Berner B.P., Bhandari D., Bolshakov S.,

RA Beson K.Y., Benos P.V., Berner B.P., Bhandari D., Bolshakov S.,

Borkova D., Botchen M.R., Bouck J., Brokstein P., Brottier P.,

RA Berloss B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Borkova D., Botcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

A de Pabloss B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

Borson K.J., Evangelista C.C., Ferraz C., Ferriera S., Pleischman W.,

RA Boston K., Doup L.E., Downes M. Dugan Rocha S., Pleischman W.,

RA Bostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

RA Harils N.L., Harvey D., Hamman T.J., Harnandez J.R., Houck J.,

A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Morris J., Moshrefi A.,

Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Rabarzolo M., Dittaman G.S., Pan S., Pollard J., Wall P., Rabarzolo M., Pittaman G.S., Pan S., Pollard J., Wall P., Rabarzolo M., Pittaman G.S., Pan S., Pollard J., Wang X.,

Rabic B.C., Siden-Klamos I., Simpson M., Strong R., Walsenberd J.,

Rabic B.C., Siden-Klamos I., Simpson M., Strong R., Walsenberd J.,

Rabic B.C., Shork E.W., Niton K., Wun Strong S., Yao Q., A.,

Walliams S.M., Woodage T., Worley K.C., Wu D., Yur Y., Walley R., Williams S.M., Woodage T., Worley K.C., Wu D., Yen S., Zhon G., Shore, Zhore, Zhon B., Zhon G., Shore, Zhon G.
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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RKAINTEMENTELEZ;
RKAINTEMENTELEZ;
RAGENER Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Borler B.D.,
RA Button R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Apbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Apbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Barman B.P., Bhandrai D., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Brockstein P., Botcher P.,
Borkova D., Botchan M.K., Bouck J., Brockstein P., Brottier P.,
Borkova D., Botchan M.K., Bouck J., Brockstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Borkova D., Delcher A., Denng Z., Mays A.D., Dew I., Dietz S.M.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dorbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
R. Posler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
A Jalai M., Kalush F., Karpen G.H., Re Z., Kennison J. A.,
A Jalai M., Kalush F., Karpen G.H., Re Z., Kennison J. A.,
A Jalai M., Kalush F., Karpen G.H., Re Z., Kennison J.,
A Liu X., Mattei B., McIntosh T.C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RODER M., Mount S.M., Moy M., Murphy L., Murphy L., Masny D., D.
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                                                                                                                       58 VIQTIEVMKQTEVLQSLIETYSNKN----GSSNYLLNPCLMIP------EVDFPP 102
                                                                                                                                                                                 123 PNAPFQI---RHSDP-----ESDFYRGKGEPVTELSWHSCRQLLYQAVATILAHAGFD 172
                                                                                                                                                                                                                                 103 ENAAELVGSQKFQKPIWFTPTVDTAYSRGDPEAYPEIPSSACRQAMRKVMCGMLRLAGFT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GSTGSSGTVSSQQMLYGLLDGQ 322
                                                                                           63 TIHTIQLIQHNRRLRNLIATAQAQNQQQTEGVKTEESEPLPSCPGSPPLPDDLLPLDCKN 122
    62
                                                                                                                                                                                                                                                                                                      163 DCSESAVQLLTDATEEFLRSFIGEYRGYYDSQPRLQNS---TVLQLVPLERAHFAQTGT-
YWGEIPISSSQTNRSSFDLLP---REFRLVEVHDPPLHQPSANKPKPPTMLDIPSEPCSL
                                           5 HWGSLPAEDDGGQLTPDKYVPTAAKKLKLDEIRQRGDPQPQEKHHK----LELRS---AL
                                                                                                                                                                                                                                                                            173 CANESVLETLTDVAHEYCLKFTKLLRFAVDREARLGQTPFPDVMEQV-----FHEVGIG
                                                                                                                                                                                                                                                                                                                                                                     SVLSLQKFWQHRIKDYHSYMLQISKQLSEEYERIVNPEKATEDAKPVKIKEEP---VSDI
                                                                                                                                                                                                                                                                                                                                                                                                                219 SLTQVHNYYKHKVLARNRAEIAEFNSVLQEYDKLMKESQSSMQKQHNEFNGHDFLNILDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 TFPVSEELEADLASGDQSLPMGVLGAQSERFPSNLEVEASPQASSAEVNASPLWNLAHVK
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Eukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         279 SATGSSQSIGGMAMGDMLQDLG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      344 MEPQESEGNVSGHGVLGSD 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Sinpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Syirskas R., Pector C., Turner R., Venter E., Wang A.H., Wang X.,
Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
R. J., Yeh R.-F., Zaveri J.S., Zhan M., Zhong G., Zhao Q., Zheng L.,
A Gibbs R.A., Myers E.W., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Cibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
Exence 287:2185-2195(2000).
Exelone 287:2185-2195(2000).
Exelone 287:2185-2195(2000).
Exelone 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                        13 SSSQTNRSSFDL-LPREFRLVEVHDPPLHQPSANKPKPPTMLDIPSEPCSLTIHTIQLIQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   468 TSTKTSKVNSQLELP--LKIVAKHEAPTEFKKIFNPIPPSELQSSKKDTKL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 HNRRLRNLIATAQAQNQQQTEGVKTEESEPLPSCPGSPPLPDDLLPLDCKNPNAPF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RQLLYQAVATILAHAGFDCANESVLETLTDVAHEYCLKFTKLLRFAVDREARLGQTPFPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        615 PEL-----SSATKSSQEEVLAMLSSPS-----DKKGHIGINEKGQLDTTGSAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 VMEQVFHEVG-IGSVLSLQKFWQHRIK-----DYHSYMLQISKQLSEEYERIVNPEKATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAKPVKIKEEPVSDITFPVSEELEADLASGDQSLPMGV------LGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        716 SAKSDKNDEKHVELKSFDLAQKVSSFVKSADKS---GIKNDATQKPQRFKKGESSSKVKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 QSERFPSNLEVEASPQASSAEVN-----ASPLWNLAHVKMEPQESEEGNVSG
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=EL TOR N16961 / SEROTYPE 01;
MEDLINE=20406833; PubMed=10952301;
Heiddelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
                                                                                                                                                                                                                                                                                                                           Ouery Match 6.0%; Score 131; DB 5; Length 1049; Best Local Similarity 19.1%; Pred. No. 0.098; Matches 89; Conservative 71; Mismatches 174; Indels 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HGVLGSDVFEEPMSGMSEAGIPQSPDDSDSSYGSHSTDSLMGSSPV 402
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Last annotation update)
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(TrEMBLrel. 15, Last sequ
(TrEMBLrel. 19, Last anno
protein VC0998.
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VC0998.
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Q9KTA5
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55613 MW; 4E88D0BBA42383E7 CRC64;

505 AA;

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                                                                                                                                                                                                                                                                                                                                      167 AHAGFDCANESVLETLTDVAHEYCLKFTKLLRFAVDREA--RLGQTPFPDVMEQVFHEVG 224
                                                                                                                                                                                                         Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.;
                                                                                                                                                                                                                                                               LNDLELPEENDEPQLAEVTPSSAFDEQQVETEIEPESEPLAAEASNDESDLTALNELDLP
                                                                                                                                                                                                                                                                                         ----DDLLPLDCKNPNAPFQIRHSDPESDFYRGKGEPVTELSWHSCRQLLYQAVA--TIL
                                                                                                                                                                                                                                                                                                               EYTEEDVLADVQLEPAAESEV---EPDLELV---NEPVTEEAFTELDELDLPEYTEEDAL
                                                                                                                                                                                                                                                                                                                                                             979 ADAQLEPVAESEVEPELDLASE------PAEEEAFTELNKLDLPEYTEE----
                                                                                                                                                                                                                                                                                                                                                                                                                                    -----KPVKIKEEPVSDITFPVSEELEADLASGDQSLPMGVL--GAQSERFPSNLEVEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                1080 ESEVEPELELVSEPVTEEAFTELDELDLPEYTEEDALADAQLEPAVESEVEP-ELELASE
                                                                                                                                                                                            9 EIPISSSQTNRSSFDLL----PREFRLVEVHDPPLHQPSANKPKPPTMLDIPSEPCSLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P--QASSAEVNASPLWN-----LAHVKMEPQESEEGNVSGHGVLGSDV-FEEPMSGMSE
                                                                                                                                                                                                                                                                                                                                                                                    225 IGSVLSLQKFWQHRIKDYHSYMLQISKQLSE----EYERIVNPEKATEDA-----
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                                                   "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.";
                                                                                                                                                                      92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                               Length 1621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Nyakatura G., Mewes H.W., Mannhaupt G.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                      Indels
                                                                                                                         2EF38BAC27A2485D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             German Neurospora genome project;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ALG/0009; CAD21385.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                           5.8%; Score 126; DB 16;
21.7%; Pred. No. 0.46;
iive 75; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               505 AA
                                                                                                                                                                   75; Mismatches
                                                                                                           protein; Complete proteome.
621 AA; 178073 MW; 2EF38B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                         Nature 406:477-483(2000).
EMBL; AE004181; AAF94159.1; -.
TIGR; VC0998; -.
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                                                                                                                                                                     93; Conservative
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                                                                                                                       1621 AA;
                                                                                                                                                          Local Similarity
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                                                                                                            Hypothetical
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                                                                                                                         SEQUENCE
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                                                                                                                                             Query Match
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Q8X0V8;
                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 NAPFQIRHSDPESDFYRGKGEPVTELSWHSCRQLLYQA-VATILAHAGFDCANESVLETL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : |: : |: : | : : | 3.4 | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... 
                                                                                                                                                                                                                                                                                                                                                                                                                                           70 IQHNRRLRNLIATAQAQNQQQTEGVKTEESEPL---PSCPG--SPPL-PDDLLPLDCKNP 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVPAGGE-----VEPPWALKGSPLRAEDAFSGSNGSAGVVSSS-----KNAGHIGOO 391
                                                                                                                                                                                                                                                                                                                10 IPISSSQTNRSSFDLLPREFRLVEVHDPPLHQPSANKPKPPTMLDIPSEPCSLTIHTIQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 TDVAHEYCLKFTKLLRFAVDREARLGQTPFPDVME-------QVFHEVGIGS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---WQHRIKDYHSYMLQISKQL---SEEYERIVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 YMRVLGYSRIPVFTGAPDGGSGEQSGACQWQPQPSDCVYFALEVKKRVTVPNSEQQPWYQ
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Ligter N., Latreille P.,
Lightning J., Lloyd C., McMurray A., Mortinore B., O'Callaghan M.,
Barsons J., Percy C., Rifken L., Staden R., Saunders D., Shownkeen R.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                101;
                                                                                                                                                     Indels
                                                        Length
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Last annotation update)
                                              5.6%; Score 121.5; DB 3;
ilarity 17.7%; Pred. No. 0.2;
Conservative 69; Mismatches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2957 AA
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MEDLINE-94150718; PubMed-7906398;
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STRAIN=BRISTOL N2;
Davidson S., Wohldmann P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---VLSLOKF--
Query Match
Best Local Similarity
T6; Conserva
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SEQUENCE FROM N.A.
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Ephydroidea; Drosophilidae; Drosophila
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                                                                                                                                                                                                                                                                                                                                    85 AQNQQQTEGVKTEESEPLPSCP----GSPPLPDDLLPLDCKNPNAPFQIRHSDPES---- 136
                                                                                                                                                                                                                                                                                                                                                                                     185 QAGQQQAQG--PPGYGPYGYAPQASTGYPPPSQQSPY-APQAGPPPQMRHQYPPHSQQQ 241
                                                                                                                                                                                                                                                                                                                                                                                                             -----DFYRGKGEPVTELSWHSCRQLLYQAVATILAHAGFDCANESVLETLTDVAHEYC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKFTKLLRFAVDREARLGQTPFPDVMEQVFH-----EVGIGSVLSLQKF-----WQ 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------EQWGRVGTNDLMNVIAQVEKSSAECKARIQQLYNMQRSASADAEVQQLQ 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237 HRIKDYHSYMLQISKQLSE-EYERIVNPEKATEDAKPVKIKEEPVSDITFPVSEELEADL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HKLAQFQSDHYRYSQQLQHVQWQQQQQQQQAAAAA-------AAAAAAAS 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                296 ASGDQSLPMGVLGAQSERFPSN---LEVEASPQASSAEVNASPLWNLAHVKMEPQESEEG 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             353 NVSGHGVLGSD-----VFEEPMSGMSEAGIPQSPD-----DSDSSYGSHSTDSLM 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | |---GYGGAGSGASSTESKESIVPPEPTPSMQESPVPNAPQVKMEPEKPSPYQQQYNGMEN 483
                                                                                                                                                                                                                                                                                                                     37 PPLHQPSANKPK------PPTMLDIPSEPCSLTIHTIQLIQHNRRLRNLIATAQ 84
                                                                                                                                                                                                                                                                                                                                                                                                                                 242 APPGYWDGYQGYGGPPPS-----QQQQQGGGPVTAPQSMQMAQQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       374 AGCHHOGPPPPTSSQSNQIPSNPNSVPVHVNQPGSQVHITADKTRILISVYHD-----
                                                                                                                                                                                                                                                                                                Indels 127; Gaps
                                                                                                                                                                                                                                                                          Length 2957;
                                                                                                                                                                                                                                                   2957 AA; 325734 MW; 33DCE1D0F60E9DDE CRC64;
"The sequence of C. elegans cosmid T04D1."; Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                      Waterston R.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF067617; AAC17559.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                44; Mismatches 172;
                                                                                                                                                                                                                                                                         DB 5;
                                                                                                                                                                                                                                                                                     Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 2977 AA.
                                                                                                                                                                                                                                                                          Score 121.5;
                                                                                                             InterPro; IPR001650; Helicase_C.
InterPro; IPR001005; Myb_DNA_binding.
InterPro; IPR000330; SNF2_N.
Pfan; PF00271; helicase_C; 1.
Pfan; PF00176; SNF2_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OYAAP9;
01-MAY-2000 (TIEMBLrel. 13, Created)
01-MAY-2000 (TIEMBLrel. 13, Last seq
01-DEC-2001 (TIEMBLrel. 19, Last ann
                                                                                       InterPro; IPR000953; Chromo.
                                                                                                                                                                                                                                                                         5.6%;
                                                                                                                                                                                                               PROSITE; PS50013; CHROMO_2;
PROSITE; PS50090; MYB_3; 1.
                                                                                                                                                                                                                                                                                     Similarity 20.0%;
                                                                                                                                                                                           SMART; SM00490; HELICC; 1.
SMART; SM00395; SANT; 1.
                                                                                                                                                                                                                                                                                              86; Conservative
                                                                                                                                                                    SMART; SM00298; CHROMO; 2
SMART; SM00487; DEXDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          398 GSSPVFNQR 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSGNPYAQQ 492
                                                                                                                                                                                                                                        Helicase.
                                          STRAIN-BRISTOL N2;
                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CG11873 protein.
                                                                                                                                                                                                                                       ATP-binding;
                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       191
                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                          132
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RAMEDLINE-2019900; PumbRed-10,1113;

RA Admans N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Holt R.A., Evans C.A., Galle R.F.,

Ramadrides P.G., Scherer S.E., Holt R.A., Evans O., Champe M. Pfeiffer B.D.,

RA Amanatides P.G., Scherer S.E., Richards S., Abburner M., Henderson S.N.,

B. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

B. Bardon R.C., Rogers Y. H.C., Blazed; R.G., Champe M. Pfeiffer B.D.,

RA Abrill J.F., Agbayani A., An H.-J., Andrews-Frankchof C., Baddwin D.,

B. Ballew R.M., Basu A., Baxendale J., Bayaktarogiu L., Beasley E.M.,

B. Barkova D., Botchan M.R., Bouck J., Brokstein D., Brotlakov S.,

B. Borkova D., Botchan M.R., Bouck J., Brokstein D., Brotlakov S.,

RA Burtis K.C., Bausm D.A., Buller H., Gadleu E., Center A., Chandra I.,

Cherry J.M., Cavaley S., Dahlke C., Davenport L.B., Davies P.,

RA Burtis K.C., Bausm D.A., Buller H., Galdeu E., Center A., Chandra I.,

Cherry J.M., Cavaley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K., Doup L.E., Downer M., Dugarn-Rocha S., Dunkov B.C.,

B.D., Darchen M.R., Bouck J., Hernandez J.R., Harris M.,

B.D., Brotler A., Gong F., Gorrell J.H., Gu Z., Gubn P., Harris M.,

RA Fobler C., Gabriellan A.E., Garg M.S., Gelbart W.M., Glasser K.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Halman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Halman T.J., Well M.-H., Ibegwan C.,

Adalen B.E. Kodita C. D., Kraft C., Kraritz S., Kulp D., Lai.

RA Liu X., Mattel B.M., McIntoly H., Murphy L., Murphy L.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Murphy B.,

Rainer R.M., Matten G.S., Pan S., Pollard J., Puri V., Reathert R.,

Rainer R.M., Nelson K.N., Navon K., Nusskern D.R., Sun E.,

Spier E., Spradling A.C., Turner R., Venter J.C., Scheeler F., Shen H.,

Spier E., Stradling A., Tundling M., Zhong K., Sun E.,

Rainest R.M., Woodage T., Wentser D.W., Zhong W., Zhong S., Yan S., Pan 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2077 NIHNSNSAMQVNNMILPILPPIQPQQQPQPQIQQPPTPILPPVAPTMAMGVAPGPMGNLVPS 2136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2137 LPTIPSLP---LYMPSKMDEMPTQKPKIARLSLFVR-----QLEVDQESCLKPDYVKPFR 2188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2189 TKDEAVKRLIR---YHCMHENDVELPSD-------EDEEFESTALEFQDKF 2229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---QAVATILAHAGFDCANESVLETLTDVAHEYCLKFTKLLRFAVDREARLGQTPFPDVM 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 EQV---FHEVGIGSVLSLQKFWQHRIKDYHSYMLQISKQLSEEYERIVNPEKATEDAKPV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 QTNRSSFDLLPREFRLVEV-----HDPPLH--QPSANKPKPPTMLDIPSEPCSLTIHTI
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tive 58; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5;
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MEDLINE=20196006; PubMed=10731132;
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[1] SEQUENCE FROM N.A.
Laird G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                83;
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Best Local 9
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                                            09ER99
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ID Q9Y4V2
                      RESULT 12
Q9ER99
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2328 IKNSADVNK-----AFSKSQPQQTTTVKQEESNESGEPSVNGSVKSEGHDKESSKYIKK 2381
                                                     281 OLKEEQTSE----KSTAESDVLSEAK-----VKEEIKQEPIDKSAQPDGVVDKFDL 2327
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                                                                            379
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                                326
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                                                                           327 --SSAEVNASPLWNLAHVKMEPQES-----EEGNVSGHGVLGSDVFEEPMSGMSEAGIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KPKPPTM------LDIPSEPCSLTIHTIQLIQHNRRLRNLIATAQAQNQQQTEGVKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326 KPKPRALCKQLSDAASTELPESP------LEAPQISSLLDADPVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EE----SEPLPSCPGSPPL------PDDLLPLDCK--NPN-APFQIRHSD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             366 PSAEAPSEPKPAAKDSPTKKXGVHKRSQHQGPDDIYLDDLKALEPEVAALYFPKSDTDPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----PESDFYRGKGEPVTELSWHSCRQLLYQAVATILAHAGFDCANESVLETLTDVAHEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  426 SRQWPESDIFSGSQSP------QSVGSAAADSGTECLSDSAMD-LPDVTLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C------LKFTKLLRFAVDREARLGQTPFPDVMEQVFHE-----VGIGSVLSLQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     471 CGGLSENGEISKEKFMEHIITYHEFAENPGLIDNPNLVIRIYNRYYNWALAAPMILSLQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---TEDAKPVKIKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              531 FQK------SLPKATVESWVKDKMPKKSGRWWFWRKKESMIKQLPETKEGKSEVP
                                KIKEEPVSDITFPVSEELEADLASGDQSLPMCVLGAQSERFPSNLEVEASPQA - - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=20578762; PubMed=11138012;
Peterfy M., Phan J., Xu P., Reue K.;
"Lipodystrophy in the fld mouse results from mutation of a new gene encoding a nuclear protein, lipin.";
Nat. Genet. 27:121-124(2001).
EMBL; AF286723; AAG52761.1;
                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 WGEIPISSSQTNRSSFDLLPR-----EFRLVEVHDPPLHQPSAN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         580 PANDLPSNAEEPTSARPAENDTSSDEG-----SQELEESIKVD 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVSDITFPVSEELEADLASGDQSLPMGVLGAQSERFPSNLEVE 321
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; ARECOLES, MISSONISS, MOSTELED.
INTERPRO; IPRO01395; Aldo/ket_red.
INTERPRO; PR00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
FROMIFICE 893 AA; 99617 MW; 3ADCOC240626B574 CRC64;
                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.5%; Score 120.5; DB 11;
18.9%; Pred. No. 0.54;
ive 52; Mismatches 136;
                                                                                                                                                                                                    AA
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                                                                                                                                                                                                    893
                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
                                                                                                                                          DYDNFD 2387
                                                                                                                      380 SPDDSD 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 76; Conserv
                                                                                                                                                                                                                                  01-JUN-2001
01-MAR-2002
                                                                                                                                                                                                                       01-JUN-2001
                                                                                                                                           2382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SERFPSNLEVEASPQASSAE-VNASPLWNLAHV-KMEPQESEEGNVSGHGVLGSDVFEE 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265 HLASDNPTMEVETLQSNPSCEPVEHSILTRELQLPEDNVDMSTMDNKDDNSSLLSGHGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --TEGVKTEESEPLPSCPGSPPLPDDLLPLDCKNPNAPFQI----RHSDPESDFYRGKGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVTELSWHSCRQLLYQAVATILAHAGFDCANESVLETLTDVAHEYCLKFTKLLRFAVDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 ARLGQTPFPDVMEQVFH----EVGIGSVLSLQKFWQHRIKDYH-----SYMLQISKQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----PASEESPEHVTCQSEIGAESQPSVSDLSGRRVQSVHLTPSDQYSQGSCHQAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 HQPSANKPKPPTMLDIPSEPCSLTIHTIQLIQHNRRLRNLIATAQAQNQQQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSVESAEEFC------SVTVALKEL-HELLVISCK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SESGKTEIVGTAPCAAVEDEASTSF - - EGLGDGLSPDREDVRRSTESARKSCSVAITSAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurons
                                                                                                                                                       Muš musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162; Indels 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 11; Length 582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DJ437M21.3 (Protein kinase C and casein kinase substrate in (Fragment).
                                                                                                                                                                                                                                                                                                                    Baumgarten K., Gorboulev V., Koepsell H.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases
EMBL; Y11917; CAA72676.1; -.
InterPro; IPR000449; UBA_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00165; UBA; 1. SEQUENCE 582 AA; 61247 MW; 23CB8C50CA2B390F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PMSGMSEAGIPQSPDDSDSS-----YGSHSTDSLMGS 399
                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGAGLPRSGLDQPPTQSLSTPSVLPPFIFPAADVDRILGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.4%; Score 118.5; DE 20.8%; Pred. No. 0.43;
AA
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582
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PRT;
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                                                                                                                              Regulatory subunit of SGLT1
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
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207 KYEKSL----KELDQGTPQYMENMEQVFEQ--
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EMBL; AF110520; AAC97966.1; -.
EMBL; AK002623; BAB22238.1; -.
                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                         11|: |:|
409 STDANGDSNP 418
                                                                                                                                                                                                                    392 STDSLMGSSP 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                  252 QLS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339 LAHVKMEPQESEEGNVSGHGVLGSDVFEEP-----MSGMSEAGIPQSPDDSDSSYGSH 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 ----YNPFEDEDDT-----GSTVSEKDDTKAKNVSSYEKTQSYPTDWSDDESNNPFS 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 KFTKLLRFAVDREARLGQTPFPDVMEQVFHEVGIGSVLSLQKFWQHRIKDYHSYMLQISK 251
                                                                                                                                                                                                                                                                                                                                                                                           252 QLS-----EEYERIVNPEKATEDAKPVKIKEEPVSDITFPVSEELEADL----
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

1. SIMILARITY: CONTAINS 1 SH3 DOMAIN.
EMBL; ALO49758; CAB51395.1; -.
HSSP; Q60631; LGBQ.
InterPro; IPR001060; Cdc15_Fes_CIP4.
InterPro; IPR001452; SH3.
InterPro; IPR00452; SH3.
PRINTS; PR00452; SH32 1.
PRINTS; PR00452; SH32 1.
SMART; SM00266; SH3; 1.
ROSITE; PS50002; SH3; 1.
RNOSITE; PS50002; SH3; 1.
RNON_IER
                                                                                                                                                                                                                                               Match 5.4%; Score 117; DB 4; Length 335; Local Similarity 22.8%; Pred. No. 0.26; les 57; Conservative 32; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.4%; Score 117; DB 4; Length 486; 22.8%; Pred. No. 0.44; tive 32; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC008037; AAH08037.1; -
InterPro; IPR001060; Cdc15_Fes_CIP4.
InterPro; IPR001452; SH3.
Pfam: PF00011; FCH;
Pfam: PF00011; FCH;
Pfam: PF00018; SH3; 1.
                                                                                                                                                                                                                    335 AA; 37945 MW; 895A94D996CA3582 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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Homo sapiens (Human).
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PROSITE; PS50002; SH3; 1.
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Best Local Similarity 22.8%
Matches 57; Conservative
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RP SEQUENCE FROM N.A.

RR SEQUENCE FROM N.A.

RR SEQUENCE TISSUE=KIDNEY;

RX MEDIINE=21085660; DubMed=11217851;

RA Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Shibata K., Xonno H., Adachi J., Fukuda S.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Flutono M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Gustincich S., Ribora M., Sachoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Sazuki H., Zoyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Rohtsuki S.,

Lyose P., Sari R., Rasegawa Y., Kawaji H., Rohtsuki S.,

Raseli R., Rasegawa Y., Kawaji H., Rohtsuki S.,
                                                                                                                                                                                                                                                                               ----COOFEEKRLRFFREVLLEVOK 253
                                                                                                                                               296 -------ASGDQSLPMGVLGAQSERFPSNLEVEASPQASSAEVNASPLWN 338
                                                                               339 LAHVKMEPQESEEGNVSGHGVLGSDVFEEP-----MSGMSEAGIPQSPDDSDSSYGSH
                                                                                                                                                                              : | | | : | | | : | | 314 RREKKKATDGVTLTGINQTGDQSLP-----SKPSSTLNVPSNP-AQSAQSQS----
                                                ---EEYERIVNPEKATEDAKPVKIKEEPVSDITFPVSEELEADL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
NG28 (Adult MALE kidney CDNA, RIKEN FULL-length enriched LIBRARY, clone: 0610013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rowen L., Oin S., Madan A., Loretz C., Hall J., James R., Dors M. Shaffer T., Abbasi N., Ratcliffe A., Dickhoff R., Lasky S., Hood "Sequence of the mouse major histocompatibility complex class II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR0002110; ANK.
InterPro; IPR000209; Peptidase_S8.
Pfam; PF00023; ank; 5.
SMART; SM00248; ANK; 3.
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120 PRSLSRNPRVEHTLLETSRRLEGAQARERALSPARAVTRSPRGSGRSSPAPNPALASPG- 178
                                                                                                                                                                                                                                                                              59 PCSLTIHTIQLIQHNRRLRNLIATAQA--QNQQQTEGVKTEESEPLPSCPGSPPLPDDLL 116
                                                                                                                                                                                                                                                                                                             117 PLDCKNPNAPFQIRH------142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----RELEE 380
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235 EIEAR-PDKLAQLRRLTERLATSDRGVRSRASPRAEDPDGLAARRSEGALQVLDPGSRTP 293
                                                                                                                                                                                                                                                                                                                                                                                                                                        143 -GEPVTELSW----HSCRQLLYQAVATILAHAGFDCANESVLETLTDVAHEYCLKFTKLL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   294 DGEPRIRETGTEVPETREVDAQAVPE-TGEAGVEVVPETV-EVDIWVIEE-----LL 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 RF--AVDREARLGQTPFFPDVMEQVFHEVGIGSVLSLQKFWQHRIKDYHSYMLQISKQLSE 255
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                                                                                                                                                                                                  11 PISSSQTNRSSFDLLPREFRL--VEVHDPPLHQPSA-----NKPKPPTMLDIPSE 58
                                                                                                                  Query Match

5.4%; Score 116.5; DB 11; Length 791;
Best Local Similarity 21.6%; Pred. No. 0.96;
Matches 100; Conservative 57; Mismatches 146; Indels 161; Gaps
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PROSITE; PS50088; ANK_REPEAT; 3.
PROSITE; PS50297; ANK_REP_REGION; 1.
PROSITE; PS00136; SUBTILASE_ASP; UNKNOWN_1.
ANK repeat; Repeat.
SEQUENCE 791 Aa; 84185 MW; 6BB5307AEEDDB3E6 CRC64;
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Title: Perfect score:

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B1770385 603055622
B0576180 UI-HE21-
B6489862 60218753
BM728984 UI-E-E01-
B0687224 AGENCOURT
B1763619 603050193
B11855674 60338302
B1193419 602947051
B6149842 nae01c08.
B1160260 6022663964
B6759070 AL559070
B1602617 603248445
B1602617 603248445
B1602617 60348445
BM802810 AGENCOURT
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BM802810 AGENCOURT
BM802806 AGENCOURT
BM802810 AGENCOURT
BM902810 AGENCOURT
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BA310780 1948611.y
B1907412 603063781
BG927465 HNC54-1-A
BC033451 602301836
BE280681 601155947
BM748747 K-EST0023
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BF947767 MR3-NN022
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BG705505 602688609
BE292913 601105354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKO12134.1 GI:12848691
HTC; CAP trapper.
Mus musculus (strain:C57BL/6J) 10 days embryo cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:2610524B01.
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinse; Mus.
                                                                                                                                                                                                                                                                                                                                           AL580770 AL580770
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enriched library, clone:2610524B01:homolog to ANTIGEN ART1/P17,
full insert sequence.
         BI669780
BM468753
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
9279253
10349636
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                                                 BQ576180
BG489862
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BM728984
BIJ3619
BIJ5674
BIJ3419
BIJ160560
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BM989602
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BQ576180
                                                                                                                                                               AL559070
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BM802810
BM050170
BM802006
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BG776075
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BM310780
B1907412
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SOURCE
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AUTHORS
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                                                                                (without alignments)
10820.179 Million cell updates/sec
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                                                                                                                                 1711
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                                                                                                                                July 18, 2003, 07:40:17; Search time 2561 Seconds
                                                                                                                                                                                                        32308132
         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                  16154066 seqs, 8097743376 residues
                                                                                                                                                                                                    Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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1057 940.4 904.6 824.4 817.4 797.4

Score

No.

REFERENCE AUTHORS MEDLINE PUBMED REFERENCE AUTHORS

JOURNAL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTCCCTCGTGCCCTGGGTCACCTCCTCTCCTGATGACCTCCTGCCTTTAGATTGTAAG
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2598. .2603
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Snibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Gemomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://maqg.llnl.gov
Plate: LLAM12787 row: f column: 22
High quality sequence stop: 674.
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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source anonymous pool of 6 male brains, age range 23-27; male lung, age 27; and 1 male testis, age 69. Library is oligo-dr primed and directionally cloned (Ecork site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH, MGC Library.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGCAGCAGACAGAAGGTGTAAAAACTGAAGAGAGTGAACCTCTTCCCTCGTGCCCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGATCCGGCACAGTGACCCAGAGAGTGACTTTTATCGTGGGAAAGGGGAACCTGTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGCCCCCCACTATGCTGGACATCCCCTCAGAGCCATGTAGTCTCCACCATACGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCACCTCCTCTCCCTGATGACCTCCTGCCTTTAGATTGTAAGAATCCCAATGCACCATTC
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                                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                                   Length 1027;
                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                             Score 940.4; DB 14;
Pred. No. 8e-162;
0; Mismatches 32; I
pCMV-SPORT6; Site_1: NotI; Site_2:
                                                                                                                                                                                                                               Query Match 55.0%;
Best Local Similarity 96.6%;
Matches 982; Conservative
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us-09-857-308-2.rst

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1150 TAAACCTGTGAAGATCAA-GGAGGAACCTGTGAGCGACATCAC-TTTTCCTGTCAGT-GA 1206
         1090 TAAGCAACTCTCTGAAGAATATGAAAGGATTGTCAATCCTGAGAAGGCCACAGAGGACGC
                                                                                                      GGAGCTGGAGGCTGACCTTGCTT 1229
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5', mRNA sequence.
BM545988
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BM545988
LOCUS
DEFINITION
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AUTHORS
TITLE
JOURNAL
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                           /tissue_type="embryonal carcinoma, cell line"
/lab_host="mbryonal carcinoma, cell line"
/lab_host="mbridge-resistant,"
/note="Organ: testis; vector: pcWv-SPORT6; Site_1: NotI;
Site_2: Sali; cloned unidirectionally; oligo-dr primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NHLMGC Library. 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 TCAGCACAACCGACGTCTTCGCAACCTTATTGCCACAGCTCAGGCCCAGAATCAGCAGCA
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLAM13291 row
High quality sequence stop: 653.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 824.4; DB 14; Length 865;
Pred. No. 1.2e-140;
0; Mismatches 2; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.2%;
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858; Conservative
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Matches 85
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ORIGIN
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of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dr primed and directionally cloned (ECORV site 1s destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. gruber (Invitrogen). Research Genetics tracking code 036.
1214 bp mRNA linear EST 20-FEB-2002
NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5588387
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                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conteact: Robert Strausberg, Ph.D.
Email: Ggapbs-rémail.nih.gov
Tissue Procurement: Invitrogen
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LimAN12559 row: g column: 12
High quality sequence start: 135
High quality sequence stop: 529.
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                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1214)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site_1: EcoRV (destroyed); Site_2: Not1; RNA source p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 2e-139;
0; Mismatches 22; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5588387"
/clone_lib="NHH_MGC_125"
/lab_host="DH10B"
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/clone="Index: 42300"
/clone="Index: 42200"
/clone="Index: 42200"
/tissue_type="large cell carcinoma"
/tissue_type="large cell carcinoma"
/tab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOPB7; Site_1: XhoI; Site_2:
FCORI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRIX/AnoI sites using the following 5' adaptor:
GGAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis XII (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGAAGAGAGTGAACCTCTTCCCTCGTGCCCTGGGTCACCTCCTCTCCCTGATGA-CCTC 685
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2600 row: c column: 19
High quality sequence stop: 635.
Location/Qualifiers
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11 Similarity 96.7%; Pred. No. 9.6e-136;
889; Conservative 0; Mismatches 21;
      lissue Procurement: DCTD/DTP/Gazdar
                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
                                                                                                     CNGCAGTGAATAGTGTGGTACCTCCTTGTCTCGGTTCAGGTCCAGACCTCCCCGTCTTCC
                            GGCTGCCCTGAACGTCAGGCGACCTCAGGACCCTGTGATTGGCGCCTGCGCCGGGGGGACCCTGTGATTGGCGCCTGCGCCGGGGGGACCCTGTGATTGGCGCCTGCGCCGGGGGGCCCCTGTGCCTTGGCGCCTGCGCCGGGGGCGCCGGGGGCCCTGTGATTGGCGCCTGCGCCGGGGGCGCCCTGTGATTGGCGCCTGCGCCGGGGGCGCCCGGGACC
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Gaps

86 9 146 120 206 266 240

326 300 386 360 446 420 506 480 566 540 626 600

180

Length 904;

Score 758.4; DB 13; Pred. No. 1.2e-128;

44.38; 95.18;

Query Match Best Local Similarity

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603293356F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5312869 5', BI669780
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                                           FGCCTGGCATTTGATAAATGTTGTTGAACTTGAAGACACATA 334
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700

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665 877 937

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InAdE:5541406"
/clone=lib="NIH_MGC_88"
/tissue_type="duodenal adenocarcinoma, cell line"
/tissue_type="duodenal adenocarcinoma, cell line"
/tab_nost="numble (phage-resistant)
/note="Organ: snall intestine; Vector: pOMV-SPORT6;
Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC_Library."
1 a 265 c 237 g 217 t 2 others
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AGENCOURT_6481158 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5541435
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                        AAGAATCCCAATGCACCATTCCAGATCCGGCACAGTGACCCCAGAGAGTGACTTTTATCGT
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://maqg.llnl.gov
Plate: LLAM12239 row.
Column: 04
High quality sequence stop: 648.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 938)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/organism="Homo sapiens"
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/tissue_type="Squamous cell carcinoma"
/tissue_type="Squamous cell carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pcWv-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Site_2: SalI; cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                                                                                                can
Email: crapber-femail.nih.gov
Tissue Procurement: James Cleaver. M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Parrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10610 row: j column: 19
High quality sequence stop: 797.
Location/Qualifiers
                                                                      Consortium (LLNL)
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Pred. No. 1.1e-123;
0; Mismatches 38;
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CCTTGCCTCAGGCCTCTCGAGGTCCAGACGCCCCCAGCCGCTCTGCGACGCAGT	188 AGGAACCCCTGGAGGGACTTGGGGATTCCTTGGGCTCCTGTTCTTCGTGCTCCT 247	326 AATGTTTGTAACTTGAAGAGACATATGGACAATGAATCTGCAAAGATACTGGGGAGAG 385 368 ATACCAATATCATCAAGCCAGACCACAGAAGTTCCTTCGATTTGCTCCCAGGGAGTTC 427	488 CCCACTATGCTGGACATCCCCTCAGAGCCATGTAGTCTCACCATACGATTCAGTTG 547	w 14 2	ESSION UI-H-EX1-bbi-i-21-0-UI SI NCI_CGAP_CA2 Homo sapiens CDNA clone UI-H-EX1-bbi-i-21-0-UI SI NCI_CGAP_CA2 Homo sapiens CDNA clone UI-H-EX1-bbi-i-21-0-UI SI NCI_CGAP_CA2 Homo sapiens CDNA clone UI-H-EX1-bbi-i-21-0-UI SI, mRNA sequence.  CESSION BQ576180.1 GI:21479497  RASION BQ576180.1 GI:21479497  RASION BQ576180.1 GI:21479497  RASION BQ576180.1 GI:21479497  RAMIMAIN BQ576180.1 GI:21479497  RAMIMAIN BQ576180.1 GI:21479497  RAMIMAIN BQ576180.1 GI:21479497  RAMIMAIN CACAP HILP://www.ncbi.nlm.nih.gov/ncicgap.  JOURNAL DUPPLISHED (1997)  FIFTLE TUMOr Gene Index  JOURNAL OURPHISHED (1997)  Email: cgapbs-r@mail.nih.gov  Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
व्यव व्यव व्यव व्यव	አ	0	40 40 40 60 60 60 60 60 60 60 60 60 60 60 60 60	Oy 6  Db 6  Qy 7  Db 7  Db 7  Db 7  RESULT 12  ROS7618070	LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT
1016 GGCAGTGTGCTCCCTCCAGAAGTTCTGGCAGCACCGCATCAAGGACTATCACAGTTAC 1075	1189 838 1247 898	RESULT 11 B1710385 B1770385 B1770385 B1770385 T71 bp mRNA linear EST 25-SEP-2001 DEFINITION 603055622F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5205245 5', mRNA sequence. ACCESSION B1770385 VERSION B1770385.1 GI:15761963 KEYWORDS EST. SOURCE human.	: M Z H Z Z D O M H	Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:  http://image.lln.gov  Plate: LLAM11514 row: k column: 06 High quality sequence stop: 768.  Location/Qualifiers  1.71  Source //Organism="Homo sapiens" /db_xref="taxon:9666" /clone = Inawan:96545" /clone = Inawan:9717	/lab_host="DH10B"

us-09-857-308-2.rst

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Score 706; DB 12;
Pred. No. 4.6e-119;
0; Mismatches 35;
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95.2%;
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AUTHORS
TITLE
JOURNAL
COMMENT
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/clone="U1-H-E21-bbi-i-21-0-UI"
/clone="U1-H-E21-bbi-i-21-0-UI"
/clone="U1-H-E21-bbi-i-21-0-UI"
/clone="U1-H-E21-bbi-i-2-Did"
/tissue__Ibp="Chondrosarcoma Grade II"
/dev_stage="Adult"
/dev_stage="Chondrosarcoma Grade II"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Left Pelvis; Vector: pT773-pac (Pharmacia)
with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
WCI_CGAP_Ch2 is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma Grade II The library
was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oilygo-dr primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT773-Pac vector: The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
#CATNAL PACE ACCORDINAL CONTAINS AND THE PACE ACCORDINAL CONTAINS AND THE
                      CDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA-YES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          964 ACAGACTCCTTTTCCTGATGTGATGGAGCAGGTATTCCATGAAGTGGGTATTGGCAGTGT 1023
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TAG_LIB=UI-H-EZ1
TAG_TISSUE=grade-2-chondrosarcoma
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Pred. No. 6.4e-120;
); Mismatches 9;
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    735
    organism="Homo sapiens"

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187 c 158 g
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1. 821
/organism="Homo sapiens"
/db_xef="taxon:9606"
/clone="lib="NIH_MGC_18"
/clone=lib="NIH_MGC_18"
/tissue_type="large cell carcinoma"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung, Vector: pOrBF); Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRIX/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    602518753F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4637293 5', mRNA sequence.
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                                                                                                          196 TGGTTCCCACTCCACTGACAGCCTCATGGGGTCCTCCCCTGTTTTCAACCAGCGCTGCAA 137
77
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: DCTD/DTPF/Gazdar
Tissue Procurement: DCTD/DTPF/Gazdar
Tissue Procurement: DCTD/DTPF/Gazdar
Tissue Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL.)
DNA Sequencing by: Incyte Genomics, Inc.
folone distribution: MGC Elone distribution information can kftp://image.llnl.gov
http://image.llnl.gov
plate: LLCM1397 row: j column: 14
High quality sequence stop: 658.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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COWMENT Contact: Soares, MB  Drogram for Rat Gene Discovery and Mapping University of Ice Rat Gene Discovery and Mapping University of Ice Rat Gene Discovery and Mapping University of Ice Rat: 319 335 8250  Fax: 310 325 8250  Fax: 310 335 8250  Fax: 310 325 8250  Fax: 310 3250  Fax: 310 3250  Fax: 310 3250  Fax: 310 3250  Fax: 310 327 8250  Fax: 310 3250  Fax: 3207 8250  Fax: 3207	Query Match         41.2%; Score 704.4; DB 14; Length 718;           Best Local Similarity         99.6%; Pred. No. 9.4e-119;           Matches 716; Conservative 0; Mismatches 2; Indels 1; Gaps 1;           Qy 395 AGAGTTCCTCGATTGCTCCCAGGGGATTCCGTCGGGAAGTCCATGACCCACC 60           Qy 455 CTGCACCACCCACGGGAGTTCCGTCGGTGGAAGTCCATGACCCACCC
2   GAGGTCCAGACCGCCCAGCCCAGCCCAGCACCAGTGAATAGTGTGGTACCTCC   61   62   TTGTCTCGGTTCAGGTCCAGCCCCCCGACCCTGAACGTCAGCGCACCT   145   1111111111111111111111111111111	Qy 684 TCCTGCCTTAGATTGTAAGATCCCAATGCACCATCAGATCCGGCACAGTGACCCAG 743

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Search completed: July 18, 2003, 09:46:46 Job time : 2572 secs
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                                                                                                                                                                                                                                                                                            AGENCOURT_8748467 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6331976 5', mRNA sequence.
BQ887284
BQ887284.1 GI:22279298
EST.
                                                                                                                                                                  GTATTCCATGAAGTGGGTATTGGCAGTGTCTCTCCCTCCAGAAGTTCTGGCAGCACCGC 1054
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                     Freeman,
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/clone="INAGE:631976"
/clone=lb="NIH_MGC_130"
/lab_host="DH10B (phage-resistant)"
/note="Organ: otocysts; Vector: pCWV-SPORT6.1.ccdb; Site_1: EcoRv; Site_2: Not1; Cloned unidirectionally. Primer: Oilgo dr. Average insert size 1.95 kb.
Constructed by ResGen, Invitrogen Corp. Note: this is
TACCAGGCAGTGGCCACAATCCTGGCCCACGGGGCTTTGACTGTGCTAATGAGAGTGTC
                        421 TACCAGGCAGTGGCCACAATCCTGGCCCACGCGGGCTTTGACTGTGCTAATGAGAGTGTC
                                                      CTGGAGACCCTAACTGATGTGGCACATGAGTATGCCTTAAGTTTACCAAGTTGCTGCGT
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Apencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
http://mage.llnl.gov
Plate: LLAM13788 row: n column: 09
High quality sequence stop: 637.
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Tissue Procurement: Mark Maconochie, Ph.D. and Nancy
Ph.D.
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/organism="Mus musculus"
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                                                                            CATTCCAGATCCGGCACAGTGACCCAGAGAGTGACTTTTATCGTGGGAAAGGGGAACCTG
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 18, 2003, 09:48:28 ; Search time 0.872038 Seconds (without alignments) 881.929 Million cell updates/sec Run on:

US-09-857-308-5 37 1 LYQAVATI 8 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	sodium-translocati	probable gamma-ada			н		Na(+)-translocatin	NADH2 dehydrogenas	hypothetical prote	hypothetical prote	triacylglycerol li	triacylglycerol li	ABC transporter (A	hypothetical prote	cag island protein	glutamate/aspartat	glutamate/aspartat	hypothetical prote	glutamate transpor	hypothetical prote		hypothetical prote	Q	excitatory amino a	glutamate transpor	glutamate transpor	glutamate transpor		hypothetical prote
SUMMARIES	ID	S51016	T41685	31	S55596	H71948	н81918	C81185	AF0393	B82893	F82292	S77776	JC4111	F83795	AE1837	C71926	S26246	S26247	T16921	JC5078	T34005	T29633	T23481	I38399	A55676	S28901	I37426	JC4262	38	T29354
	DB	7	~	~	~	~	~	~	7	~	7	~	~	7	7	~	7	7	7	7	7	7	7	7	7	7	7	7	7	7
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dР	Query	6	86.5	3	81.1	81.1	81.1	81.1	81.1	78.4	78.4	78.4	78.4	78.4	78.4	78.4	78.4	78.4	78.4	78.4	78.4	78.4	78.4		78.4	78.4	78.4	78.4	78.4	78.4
	Score	33	32	31	30	30	30	30	30	29	29	29	29	29	29	29	29	29	29	29	29	29	29	29	29	29	29	29	29	29
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Ouery Match 86.5%; Score 32; DB 2; Length 865; Best Local Similarity 87.5%; Pred. No. 41; Matches 7; Conservative 0; Mismatches 1; Indels

two-component sens	semaphorin B - mou	hypothetical prote	sensor protein evg	probable sensor fo	probable sensor fo	hypothetical prote	hypothetical prote	hypothetical prote	conserved hypothet	hypothetical prote	hypothetical 22K p		probable phenylace	qermin-like protei	hemagglutinin - Ma
E83847	148745	A84690	G65010	A91035	C85879	S15053	AE1910	G72353	E82726	C71406	180320	E86973	B75280	T12426	JC2268
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594	160	917	1197	1197	1197	1226	120	120	145	158	192	199	230	233	247
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## ALIGNMENTS

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Gaps

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probable sodium-translocating NADH dehydrogenase (ubiquinone) (EC 1.6.5.-) chain B NM C; Species: Neisseria meningitidis
C; Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C; Accession: H81918
R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre Nature 404, 502-506, 2000
A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491
A; Reference number: A81775; MUID:20222556; PMID:10761919
A; Status: preliminary
A; Molecule type: DNA
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-410 < PAR>
A; Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; FIDN:CAB84034.1; PID:g737
C; Genetics: mannageness GB:AL162754; GB:AL157959; NID:GA911
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A;Experimental source: strain J99
C;Genetics:
A;Gene: lpxK
C;Superfamily: Escherichia coli probable tetraacyldisaccharide 4'-kinase ycaH
C;Keywords: phosphotransferase
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C;Keywords: NAD; oxidoreductase
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Best Local Similarity 62.30
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Best Local Similarity 75.۰۰
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A;Gene: NMB0568
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                                                                                                                                                                                       C; Species: Cenarchaeum Symbiosum
C; Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C; Accession: T31318
R; Schleper, C.; DeLong, E.F.; Preston, C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, R.V.
A; Title: Genomic analysis reveals chromosomal variation in natural populations of the un
A; Reference number: 220994; MUID: 98422450; PMID: 9748430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable tetraacyldisaccharide 4'-kinase (EC 2.7.1.130) lpxK [similarity] - Helicobacter C.Species: Helicobacter pylori
A; Variety: strain J99
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 02-Mar-2001
C; Accession: H71948
RAIM, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
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A;Molecule type: DNA
A;Residues: 1-312 <ARN>
A;Cross-references: GB:AE001467; GB:AE001439; NID:g4154826; PIDN:AAD05884.1; PID:g415483
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A;Reference number: A71800; MUID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:U20824; NID:g695172; PIDN:AAC13789.1; PID:g695174
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
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A;Residues: 1-269 <SCH>
A;Cross-references: EMBL:AF083072; NID:93599393; PID:93599404; PIDN:AAC62709.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-307 <TEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein E2 - equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Bate: 27-Cct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
C;Accession: S55596
R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MuID:95302501; PMID:7783207
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Pred. No. 40;
1; Mismatches (
                                                                                                                                                                      hypothetical protein - Cenarchaeum symbiosum
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Best Local Similarity 85.7%;
Matches 6; Conservative
                           11111 ||
317 LYQAVRTI 324
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  1 LYQAVATI 8
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Matches
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A; Accession: F82292
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-143 < HEI>
A; Cross-references: GB: AE004155; GB: AE003852; NID: 99655127; PIDN: AAF93862.1; GSPDB: GN
A; Experimental source: serogroup O1; strain N16961; biotype El Tor
C; Genetics:
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A; Cross-references: EMBL:233059; NID:9531610; PIDN:CAA83733.1; PID:94379137
A; Experimental source: ATCC 27343
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C; Comment: This enzyme, serine esterase enzyme, is widely distributed throughout anim in fatty acids, and hydrolyses ester bonds of triacylglycerols to yield free fatty ac
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R;Bork, P.; Ouzounis, C.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, Mol. Microbiol. 16, 955-967, 1995
A;Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physi A;Reference number: S77739; MUID:96059641; PMID:7476192
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R; Rawadi, G.; Lalanne, J.L.; Roulland-Dussoix, D.
Gene 158, 107-111, 1995
A; Fttle: Cloning and characterization of the lipase operon from Mycoplasma mycoides
A; Reference number: JC4109; WUID:95309706; PMID:7789792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    triacylglycerol lipase (EC 3.1.1.3) - Mycoplasma capricolum (fragment) N,Alternate names: lipase, protein MCO73 (S.Species: Mycoplasma capricolum (S.Species: Mycoplasma capricolum (S.Species: Mycoplasma capricolum (S.Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 21-Jul-2000
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C;Date: 23-Jul-1995 #sequence_revision 19-oct-1995 #text_change 07-Dec-1999
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   A; Reference number: A82035; MUID:20406833; PMID:10952301
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Pred. No. 30;
1; Mismatches
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Pred. No. 50;
2; Mismatches
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A;Genetic code: SGC3
C;Superfamily: triacylglycerol lipase 1
C;Keywords: carboxylic ester hydrolase
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75.0%;
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62.5%;
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Best Local Similarity 75.01
المالية وفي Si Conservative
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Best Local Similarity 62.55
The Strong Conservative
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A;Residues: 1-264 <RAW>
A;Cross-references: GB:U17036
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31 LYQAPATL 38
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Cipate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
Cipate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
Cipacession: B82890
RGlass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, February 2000
A. Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min A. Reference number: A82870
A. Accession: B82893
A. Status: preliminary
A. Molecule type: DNA
A. Residues: 1-91 - GLA>
A. Residues:
                                                                                                                                                                             NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain B [imported] - Yersinia pestis (strates) Foreis: Yersinia pestis (strate: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 03-Jun-2002 C; Accession: AF0393
                                                                                                                                                                                                                                                                                                                     R. Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Ll. M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Reference number: AB0001; MUID: 21470413; PMID: 11586360
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C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C; Accession: F82292
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
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A;Molecule type: DNA
A;Residues: 1-413 <KUR>
A;Residues: 1-413 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92474.1; PID:g15981175; GSPDB:GN00175
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54;
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Pred. No.
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Best Local Similarity 87.5%;
Matches 7; Conservative (
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75.08;
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26 LYEAAATI 33
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LLQAVATI 70
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Best Local Similarity
Matches 6; Conserv
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A; Genetic code: SGC3
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                                                                                                                                                                                                                                                                                                                                                                   ABC transporter (ATP-binding protein) natA [imported] - Bacillus halodurans (strain C-12 C; Species: Bacillus halodurans C; Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 (C; Accession: F83795 R; Takani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000 Nucleic Acids Res. 28, 4317-4331, 2000 A; Reference number: A83650; MUID:20512582; PMID:11058132 A; Accession: F83795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-299 <STO>
A;Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BAB04885.1; GSPDB:GN0d
A;Experimental source: strain C-125
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A;Status: preliminary
A;Molecule type: DNA
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A;Gene: natA
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
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A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: a110245
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Pred. No. 58;
2; Mismatches
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85.7%; Pred. No. 81;
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C;Superfamily: triacylglycerol lipase 1
C;Keywords: carboxylic ester hydrolase
F;90-94/Region: conserved site
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Similarity 85.7%;
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Best Local Similarity 62.5%;
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RESULT 15

A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric p A;Reference number: A71800; MUID:99120557; PMID:9923682 A;Accession: C71926 A;Status: preliminary A;Notecule type: DNA A;Rosidues: 1-370 CARNS A;Cross-references: GB:AE001482; GB:AE001439; NID:g4155018; PIDN:AAD06062.1; PID:g415 A;Experimental source: strain J99 C;Genetics: A;Gene: cagH C;Accession: C71926 R;Alm, R.A.; Ling, L.S.L.; Molr, D.T.; King, B.L.; Brown, B.D.; Dolg, P.C.; Smith, D. ; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F. Nature 397, 176-180, 1999 ö cag island protein - Helicobacter pylori (strain J99) C;Species: Helicobacter pylori A;Variety: strain J99 C;Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 08-Oct-1999 Gaps .; 0 Length 370; Indels DB 2; 82; Query Match 78.4%; Score 29; DB Best Local Similarity 100.0%; Pred. No. 82; Matches 6; Conservative 0; Mismatches 111111 241 YQAVAT 246 us-09-857-308-2.rge

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : GenEmbl:\*

dense : GenEmbl:\*

1: gb\_ba:\*

2: gb\_htg:\*

4: gb\_om:\*

5: gb\_om:\*

7: gb\_pl:\*

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10: gb\_pat:\*

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36: em\_htg\_mam:\*
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38: em\_sy:\*
39: em\_htgo\_hum:\*
40: em\_htgo\_nus:\*
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

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AF197954	Homo sapiens ade AF197954	AF197954.1 GI:11066257	Homo sapiens.	Homo sapiens	Eukaryota; Metaz	Mammalia; Euther	1 (bases 1 to 2021)	Nishizaka, S., Go	Shichijo, S.	A new tumor-reje
RESULT 1 AF197954 LOCUS	DEFINITION ACCESSION	VERSION KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS		TITLE

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Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.

TITLE Prediction of the coding sequences of unidentified human genes. XI.
The complete sequences of 100 new cDNA clones from brain which code
JOURNAL DADA Res. 5 (5), 277-286 (1998)
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Ohara,O., Suyama,M., Nagase,T., Ishikawa,K. and Kikuno,R.
Direct Submission
Submitted (OB-OCT-1998) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,
Fax:+81-438-52-3914)
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EEPVSDITFPPVSEELEADLASGDOSLPMGVLGAQSBRFPSNLEVEASPQASSAEVNAS
PLWNLAHVKMEPQESEEGNVSGHGVLGSDVFEEPMSGMSEAGIPQSADSDSSSYGSHS
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Pred. No. 0;
0; Mismatches
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/protein_id="BAA34484.1"
/db_xref="G1:3882249"
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/clone_lib="pBluescriptII
/dev_stage="adult"
1. .4261
                                                                                                                                                                               Homo sapiens adult male brain cDNA
SK plus clone:hk04750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="hk04750"
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966 c 897 q 12:
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Homo sapiens mRNA for KIAA0764 p
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344. .1588
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Best Local Similarity 99.8%;
Matches 1692; Conservative
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Tel:81-3-5449-5286, Fax:81-3-54416)

Tel:81-3-5449-5286, Fax:81-3-54416)

Tel:81-3-5449-5286, Fax:81-3-54416)

Toko human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                                                                                               CAAGAAGAGGATGAGGAAAATATAAAAGGAAAAGGGGAGATGTTTGTCCAGACCTACT 1620
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Ly similar to
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Homo sapiens hepatoma cell_line:HepG2 cDNA to mRNA, clone_lib:HEP
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1384 AGAAAGTGAAGAAGCAATGTCTCGGCATGGTGTGCTGGCCGCAGTGATGTCTTCGAGGA
                                                                                                               AAGTGCAGAGGTAAATGCTTCTCTCTTTGGAATCTGGCCCCATGTGAAAATGGAGCCTCA
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Direct Submission
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Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Ota,T.,
Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
Nakamura,Y., Isogai,T. and Sugano,S.
URDO human cDNA sequencing project
Unpublished
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Homo sapiens CDNA FLJ20322 fis, clone HEP09455, highly
AB018307 Homo sapiens mRNA for KIAA0764 protein,
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Pred. No. 0;
0; Mismatches
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/organism="Homo sapiens"
          /db_xref="taxon:9606"
/clone="HEPO9455".
/cell_line="HePG2"
/cell_type="hepatoma"
/clone_lip="HEP"
/note="cloning vector p
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/note="highly similar
KIAA0764 protein"
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Mammalia: Butheria; Primates; Catarrhini; Hominidae; Homo.  1 (sites) AUTHORS Watanabe,K., Kumagai,A., Itakura,S., Yamazaki,M., Tashiro,H., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., TITLE Nabanura,Y., Isogai,T. and Sugano,S. TITLE JOURNAL Onpublished REFERENCE Chases 1 to 1481) Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T., Shibahara,T., Tanaka,T. and Nakamura,Y. TITLE Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Deptment of Virology; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5416) COMMENT NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert Sequencing: Research Association for Buses sequencing: DNA library	Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency). Location/Qualifiers  1. 1481 Source /organism="Homo sapiens" / Ab_xref="taxon:9606" / Clone="KATO5969" / Clone="KATO5969" / Cell_type="signet-ring cell carcinoma" / Cell_type="signet-ring	Query Match  85.2%; Score 1457.8; DB 9; Length 1481;  Best Local Similarity 99.9%; Pred. No. 0;  Matches 1459; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  QY 191 AAACCCCTGGAGGACTTGGGCTCCTTGGGCTCCTTCTCTCTC	CTGGTGGAAGTCCATGACCCACCCTGACCCACGACAACCGAAGCCGCCCCCCTGAGCCAAGCCCCCCCC
QY         841 CCACGCGGGCTTTGACTGCTAATGACAGTGTCCTGGAGACCCTAACTGGTGGCCACA           PS         1	1141 AGAGGACGCTAAACCTGTGAAGATCAAGGAGAACCTGTGAGGACATCACTTTTCCTGT	1381 AGAAAGTGAAGGGAAT 1412	Oy 1681 TGTTCTTAAAAAA 1695  Db 1712 TGTTCTTAAAAAAA 1726  RESULT 4  AK000616  LOCUS  AK000616  AK000616  AK000616  AK000616  AK00616  AK000616  AKO00616  AKO00616  AKO00616  AKO00616  AKO00616  AKO00616  AKO00616  AKO00616  AKO00616  AKOO0616  AKOONG  AKOO0616  AKOONG  AKOO0616  AKOOO0616  AKOOOO0616  AKOOOO0616  AKOOOO0616  AKOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO

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AF224759 2869 bp mRNA linear PRI 07-JAN-2001 Homo sapiens adenocarcinoma antigen ARTI/Pl7 mRNA, complete cds.

RESULT 5
AF224759
LOCUS
DEFINITION

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PKPPTMLDIPSEPCSLTIHTIQLIGHNRRLRNLIATAQAQNQQTEGVKTEESEPLPS
CPGSPPLPDDLLPLDCKNPNAPFQIRHSDPESDFYRGKGEPVTELSWHSCRQLLYQAV
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WNLAHVKMEPQESEEGNVSGHGVLGSDVFEEPWSGMSEAGIPOSPDDSDSSYGSHSTD
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Shichijo...
Direct Submission
Submitted (14-JAN-2000) Immunology, Kurume University Scho
Medicine, Asahi-machi 67, Kurume, Fukuoka 830-0011, Japan
Location/Qualifiers
                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Nishizaka,S., Gomi,S., Harada,K., Oizumi,K., Itoh,K.
Shichijo,S.
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Nishizaka,S., Gomi,S., Harada,K., Oizumi,K., Itoh,K.
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                                                                                                                                             A new tumor-rejection antigen recognized infiltrating into a lung adenocarcinoma Cancer Res. 60 (17), 4830-4837 (2000)
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llarity 99.5%; Pred. No. 0;
Conservative 0; Mismatches
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ORIGIN
ACCESSION
VERSION
KEYWORDS
                                                           ORGANISM
                                                                                                      REFERENCE
                                                                                                                    AUTHORS
                                                                                                                                                                                            MEDLINE
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                                                                                                                                                                                                                                          AUTHORS
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction, Similarity but not identity
                                                                   Euteleostomi;
Murinae; Mus
                                                                                                           1 (bases 1 to 2616)
Strausberg, R.
Direct Submission
Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing Center
Center code: BCM-HGSC
Center code: BCM-HGSC
Contact: angebcm.tmc.edu/cdna/
Contact: angebcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.I
Richards, S., Gibbs, R.A.
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                                                                      Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10;
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Pred. No. 1.8e-291;
0; Mismatches 120;
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                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Db 1464 GTGTTCAATCAGCGCTGCAG	AX013061	TION ION N DS	Σ	REFERENCE 1 (bases 1 to 1046) AUTHORS Schmitt, A., Specht, T., Pilarsky, C. TITLE Human nucleic acid seg	NAL	RES source	240	Best Local S Matches 949	Db 46 ACGCGATCCTTGCCTCAGC	Qy 61 CAGCAGTGAATAGTGTGTA	Db 106 CAGCAGTGAATAGTGTGGTA Qy 121 GGCTGCCCTGAACGTCAGGC	Db 166 GGCTGCCTGAACGTCAGGC	Qy 181 GTGACCGAGGAACCCCTGG	Db 226 GTGACCGAGGAACCCTGG Qy 241 TGCTCCTTC-GGGCAAGGA	286		Db 346 ATTGATAAATGTTTGTTGA OY 360 GGGGAGAGATACCAATATCA	Db 406 GGGGAGAGATACCAATATCA	Qy 420 GGGAGTTCCGTCTGGTGGAA	466	Db 526 CGAGCCCCCACTATICTE	540	Db 586 TTCAGTTGATTCAGCACAAG
	524 CTCACCATCCATACGATTCAGTTGAGCACAACCGACGTCTTCGCAACCTTATTGCC 583 	584 ACAGCTCAGGCCCAGAATCAGCAGCAGACAGAAGGTGTAAAAACTGAAGAGAGTGAACCT 643 	644 CTTCCCTGGTGCCCTGGGTCACCTCCTCTCTGATGACCTCCTGCCTTTAGATTGTAAG 703 	704 AATCCCAATGCACCATTCCAGATCCGGCACAGTGACCCAGAGAGTGACTTTATGTGGGG 763 	764 AAAGGGAACCTGTGACTGACTGGCACTCCTGTCGGCAGCTCCTCTACCAGGCA 823 	824 GTGGCCACAATCCTGGCCCACGCGGGCTTTGACTGTGCTAATGAGAGTGTCCTGGAGACC 883 	884 CTAACTGATGTGGCACATGAGTATTGCCTTAAGTTTACCAAGTTGCTGCGTTTTGCTGTG 943 				1064 TATCACAGTTACATGCTACAGATTAGTAAGCAACTCTCTGAAGAATATGAAAGGATTGTC 1123 	1124 AATCCTGAGAAGGCCACAGAGACGCTAAACCTGTGAAGATCAAGGAGGAACCTGTGAGC 1183	1044 AATCCCAGAAAGGCCACAGAAGACACTAAACCTGTGAAGGATCAAGGAAGAGCCTGTGAGC 1103	1184 GACATCACTITICCTGTCAGTGAGGAGCTGGAGCTTGCTTCTGGAGACCAGTCA 1243 	1244 CTGCCTATGGGAGTGCTTGGGGCTCAGAGCGAACGCTTCCCATCTAACCTGGAGGTTGAA 1303	TTACCCATTGGGGTCCTCGGGGGTCAGAGTGACGCTTCCCATCCAACCTGGAGGTGGAG	1304 GCTTCACCACAGGCTTCAAGTGCAAAGGTAAATGCTTCTTCTTTGCAATCTGGCCCAT 1363 1224 GCTTCGCCAAGGGTCCAAGTGCAAGGGTTCTTCTCTTTTGGAATCTGGCCCAT 1363 1224 GCTTCGCCAAGGGCTCCAAGTGCAAGGGTTCTCTCTCTCT	1364 GTGAAAATGGAGCCTCAAGAAAGTGAAGGCAATGTCTCTGGGCATGGTGCTGGGG 1423	1284 GTGAAAATGGAACCTCAAGAAAGTGAAGAAGGCAATGTGTGTG	1424 AGTGATGTCTTCGAGGAGCCTATGTCAGGCATGAGGAGCTGGGATTCCTCAGAGCCCT 1483	1344 AGIGAIGICIIIGAGGAGCAAIGICAGGCAIGAGCAGGGGGGGG		1544 GTTTCAACCAGCGCTGCAAGAAGAAGAAGAAAATATAAAAGGAAA 1592 
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SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
LA NUNE (DE); METAGEN GES FUER GENOMFORSCHUN
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Primates; Catarrhini; Hominidae; Homo.
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Submitted (10-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                          825
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                                                                                                                           TCCAGATCCGGCACAGTGACCCAGAGAGTGACTTTTATCGTGGGAAAGGGGAACCTGTGA 779
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Sulston, J.E. and Waterston, R. Toward a complete human genome sequence
                   GGTCACCTCCTCTCCTGATGACCTCCTGCCTTTAGATTGTAAGAATCCCAATGCACCAT
                                                                              766 TCCAGATCCGCCACAGTGACCCAGAGTGACTTTTATCGTGGGAAAGGGGAACCTGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete sequence.
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Submitted (13.UTL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
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                                                                                                                                           2 (bases 1 to 204153)
Nguyen,C., Haglund,K., Dixon,R. and Doebber,A.
The sequence of Homo sapiens BAC clone RP11-158113
Unpublished (2002)
3 (bases 1 to 204153)
Waterston,R.H.
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Homo sapiens BAC clone RP11-158113 from 2,
AC074091
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Waterston, R.H.
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Waterston, R.H.
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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P. Y., Zhaob, B., Frengen, E., Tateno, M., Catanese, J. J. and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                   clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A PCR only region exists between bases 64163 to 64357. A transposon exists in this clone that has been deleted from the finished sequence. This transposon would insert after base 38173. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actual start of this clone is at base position 1 of RP11-158113; actual end is at base position 204153 of RP11-158113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="match to EST AI370811 (NID:94149564) ta58c03.x1"
492. .800
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/note="match to EST AA649214 (NID:g2575643) ns31f01.s1"
492. 800
/note="match to EST BF516222 (NID:g11601401)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. L. MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence was finished as follows unless otherwise noted:
Dec 21, 2001 this sequence version replaced gi:16924152
                                                      Center: Washington University Genome Sequencing Center
Center code: WUGSC
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                                                                                                                                                                                                                                                                                                            not represent the
                                                                                                                       Web site: http://genome.wustl.edu/gsc
                                                                                                                                                 Contact: sapiens@watson.wustl.edu
------ Summary Statistics
Center project name: H_NH0158113
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/db_xref="taxon:9606"
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VECTOR: pBACe3.6
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                                ---- Genome Center
                                                                                                                                                                                                                                                                                                         NOTICE: This sequence may
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625726.1 GI:1347958
STS sequence; primer; sequence tagged site.
Homo sapiens STSs derived from sequences in dbEST and the Unigene
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="match to EST AV649394 (NID:99870408)" 7541. 7559
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/note="match to EST AV734630 (NID:910852175)" 7541. 7559
/note="match to EST BF516222 (NID:911601401)"
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           /note="match to EST BF817601 (NID:g12154358)" 7541. .7559
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Whitehead Institute for Biomedical Research
O cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
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Pred. No. 5.4e-105;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Thomas Hudson
                                                                                                                                                                                                       Query Match 23.8%;
Best Local Similarity 98.8%;
Matches 411; Conservative
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/rpt_family="Ar_rich"
5309. .5603
/rpt_family="L2"
5703. .5817
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                                                                              502. .703
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/note-"match to EST BF818491 (NID:g12155853)"
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note="match to EST BG679934 (NID:913911331)"
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note="similar to Homo sapiens EST BG614976
NID:913666347)"
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/rpt_family="Alu"
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/note="match to EST B
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5703. .580°
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118953

463

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119013

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119073

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119133

119193

703

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2 (bases 1 to 17398)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Glude, S., Gordy, S., Goyette, M., Graham, L., Grand-Pierre, N., Jagos, B., Heaford, A., Horton, L., Hulme, W., Iltev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Matthews, C., MacLean, C., Madonald, P., Major, J., Marquis, N., Matthews, C., MacLean, C., Madonald, P., Major, J., Murphy, T., Naylor, J., Nguyen, C., Norens, C., Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Roback, N., Ribey, R., Santos, R., Schupback, R., Saman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stans, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wayman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center clone name: 555_E_12
------ Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                        HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                                                              Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP24-555E12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: L18761
       GI:22380991
                                                                                                               (bases 1 to 173988)
                                                                                                                                                                                   (bases 1 to 173988)
                                                                                              Eutheria;
                                         house mouse.
                                                                                                                                                                      Unpublished
                                                          ORGANISM
                                                                                                                                AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1350 GGAATCTGGCCCATGTGAAAATGGAGCCTCAAGAAAGTGAAGAAGGCAATGTCTCTGGGC 1409
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Mus musculus clone RP24-555E12, WORKING DRAFT SEQUENCE, 3 ordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1470 TTCCTCAGAGCCCTGATGACTCAGATAGCAGCTATGGTTCCCACTCCACTGACAGCCTCA 1529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1530 TGGGGTCCTCCCCTGTTTTCAACCAGCGCTGCAAGAAGGATGAGGAAAATATAAAAGG 1589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="155.8 cR from top of Chr2 linkage group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       (genbank accession T48604).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 359; DB 11;
Pred. No. 2.2e-91;
0; Mismatches 1;
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                                                                                                                                                                                                                                        Tag Polymerase: 0.025 units/ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14. .38
complement(126. .143)
1 104 c 84 g
                                                                      Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
                                                                                                                                                                                                                                                                                                                                                                                                    Derived from dbEST (genbank a
Location/Qualifiers
1. .386
Primer B: TGACAGCCTCATGGGGTC
STS size: 130
PCR Profile:
                                                                                                                                                                                Template: 10 ng
Primer: each 5 pM
dNTPs: each 4 nM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.0%;
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KCl: 50 mM
Tris-HCL: 10 mM
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                                                                                                                                                                                                                                                                                                                                                                   pH: 9.3
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AC105160
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primer_bind
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HTG 24-AUG-2002

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15. [bases 1 to 522648]

15. [bases 1 to 522648]

16. [bases 1 to 522648]

17. [contents.] Nusbeum.C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastlen,V., Boyuslavkiy,L., Boukhqalter,B., Anderson,S., Barna,N., Bastlen,V., Collymore,A., Cook,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Choepel,Y., Colangelo,M., Cage,D., Galagan,J., Gardynas,S., Farro,S., Farreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardynas,S., Goyette,M., Gape,D., Galagan,J., Gardynas,C., Horton,L., Hulme,W., Tilev,I., Johnson,R., Jones,C., Kamat,A., Kalats,A., Kells,C., Labencque,K., Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Inid,G., Macton,R., Nochuc,N., Margols,N., Matthews,C., McCarthy,M., McChan,P., Margyls,J., Naylor,C., McCarthy,M., McChan,P., Margyls,P., Peterson,R., Malor,J., Naylor,C., Nicol,R., Nochuc,N., Peterson,R., Phukhang,P., Peterson,R., Santos,P., Peterson,R., Phukhang,P., Peterson,R., Schupback,R., Saman,S., Severy,P., Spencer,B., Santos,R., Schupback,R., Semman,S., Severy,P., Santos,R., Stantos,R., Shantos,R., Shantos,
AC113276 23-2648 bp DNA linear HTG 24-AUG-200
Mus musculus clone RP23-383E21, WORKING DRAFT SEQUENCE, 6 ordered
                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                   AC113276.2 GI:22475032
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                                                                                                                                                                                                                                                             Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-383E21
                                                                                                                                                                                                                                                                                                 (bases 1 to 232648)
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                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                         Jnpublished
                            DEFINITION
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                                                                                                                                                                                                                                                                                                                                                      is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 173988;
                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                     Consensus quality: 173434 bases at least Q40 Consensus quality: 173620 bases at least Q30 Consensus quality: 173701 bases at least Q20 Insert size: 151000; agarose-fp Insert size: 173788; sum-of-contigs Quality coverage: 10.8 in Q20 bases; agarose-fp Quality coverage: 9.3 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17180 17279: gap of 100 bp
17280 91748: contig of 74469 bp in length
91749 91848: gap of 100 bp
91849 173988: contig of 82140 bp in length.
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/clone_lib="RPCI-24 Male Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 20.9%; Score 356.8; DB 2; Best Local Similarity 91.1%; Pred. No. 2.5e-90; Matches 379; Conservative 0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature 17280..91748 misc_feature 17280..91748 misc_feature 91849..173988 //note="assembly_fragment" hote="assembly_fragment" a 39239 c 39867 g 47210 t ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Aug 24, 2002 this sequence version replaced gi:18997558. Contact: sequence\_submissions@genome.wi.mit.edu site: http://www-seq.wi.mit.edu Center project Information

RESULT 11 AC113276

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AC127781
AC127781.1 GI:21908156
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Rattus norvegicus
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* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 81376 81475: gap of 100 pp

* 81476 99350: contig of 17875 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 AATCIGCAAAGATACTGGGGAGAGATACCAATATCATCAAGCCAGACCAACAGAAGTTCC
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Center clone name: 383_E_21
Sequencing vector: Plasmid; via: 100% of reads
Sequencing vector: Plasmid; via: 100% of reads
Chemistry: Dye-terminator Big bye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 229769 bases at least 030
Consensus quality: 231311 bases at least 030
Consensus quality: 231821 bases at least 030
Insert size: 240000; agarose-fp
Insert size: 232148; sum-of-contigs
Quality coverage: 8.1 in 020 bases; sum-of-contigs
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117760: contig of 18310 bp in length

117761 17860: gap of 100 bp

152147 152246: gap of 100 bp

152247 194835: contig of 42589 bp in length
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/note="assembly_fragment"

99451. 117760

/note="assembly_fragment"

117861. 152146

/note="assembly_fragment"

15247. 194435

/note="assembly_fragment"

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/note="assembly_fragment"

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clone_end:SP6
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L (Dasses I to 159250)

Readrance Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alstrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbariak, J., Benton, J., Binage, H.C., Are, J.R., Ayele, M., Bonnin, D., Barbariak, J., Berton, J., Binage, H.C., Are, J. Broon, M., Bryant, N.P., Barbariak, J., Berton, J., Brinage, H.C., Are, J. Broon, M., Bryant, N.P., Barbariak, J., Bardon, J., Chacko, J., Chacko, J., Chavez, D., Carron, T.F., Carron, T.F., Carron, T.E., Carron, T.E., Carron, T.E., Carron, T.E., Carron, T.E., Ding, T., Byrd, N.C., Carron, T.C., Coyole, M.D., Dathorne, S.R., David, R., Douthwaite, K.J., Dragar, D. Edhorne, S.R., David, R., Douthwaite, K.J., Dragar, D., Douthwaite, C., Edgar, D., Edgar, D., Edgar, D., Edgar, D., Edgards, C.C., Elhaj, C., Escotto, M., Ealls, T., Ferraguto, D., Flagg, M., Ford, J., Foster, P., Frantz, P., Gabisi, A., Garcia, A., Garrer, T., Garza, N., Haniton, K., Harris, K., Hart, M., Haves, A., Hamiton, K., Harris, K., Hart, M., Haylak, P., Hawes, A., Henindez, J., Homsi, P., Martin, R., Ma, J., Jacobson, E., Jail, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Kovah, J., Kovar, C., Ill, J., Liff, T., Liff, T., Liff, Large, O., Lieu, C., Liu, J., Liu, M., Lollias, M., Maylon, P., Martin, R., Ma, J., Maylon, N., Morgan, M., Mosed, R., Martin, R., Ma, J., Martin, R., Ma, J., Martin, R., Ma, J., Martin, R., Ma, J., Martin, R., Maylon, P., Martin, R., Mador, M., Mokuon, G., Craguo, R., Mill, J., Martin, R., Martin, R., Martin, R., Martin, R., Maylon, M., Okunon, G., Craguo, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Mangue, M., Woledo, R., Paton, B., Petry, J., Petrez, L., Peters, L., Pickens, R., Primus, E., Pull. L., Quiles, M., Rolas, A., Rolubokan, I., Rolfe, M., Rulz, S., Savery, G., Scherer, S., Scott, G., Shark, T., Waylon, W., Yungaria, A., Tamerisa, K., Tang, H., Wall, M., Charlin, S., Wall, M., Charlin, S., Wall, M., Charlin, S., Wall, M., Y., Walliams, G., and Gibbs, R. ACL2/781 155250 bp DNA linear HTG 19-JUL-2002 Rattus norvegicus clone CH230-46303, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 59 unordered pieces. 583 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; CTCACCATCCATACGATTCAGTTGAGCACCAACCGACGTTTGGCAACCTTATTGCC ACAGCTCAGGCCCCAGAATCAGCAGCAGACGAGGAGGTGTAAAAACTGAAGAGTGAACCT

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AL Unpublished

SR Worley, K.C.

Direct Submission

AL Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Center: Baylor College of Medicine

Center: Baylor College of Medicine

Center: Baylor College of Medicine

Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

Contact: hgsc-help@bcm.tmc.edu

Contact: ngsc-help@bcm.tmc.edu

Contact: ngsc-help@bcm.tmc.edu
                                                                                                                                                                                                            NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 59 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                     Center project name: GZSG
Center clone name: GTS30-46303
Center clone name: GTS30-46303
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 88645 bases at least Q30
Consensus quality: 100316 bases at least Q20
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Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Angulano, D., Angulae., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Anguleeth, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranalke, D., Barcher, M., Baranstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Bulardy, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Clacko, J., Chavez, D., Chen, G., Copte, M., Cree, A., D. Souza, L., Davila, M.L., Davis, C., Coyle, M., Cree, A., D. Boerich, D., Delgado, O., Denson, S., Deramo, C., Coyle, M., Cree, A., D., Divya, K., Draper, H., Dugan, Rocha, Carrell, L., De Anda, C., Povya, K., Draper, H., Dugan, Rocha, S., Dunn, A., Dutzhin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Elgene, C., Evans, C.A., Falls, T., Fan, G., Fraser, C., M., Gablsia, A., Garte, A., Garter, M., Guerra, W., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Gebregeorgis, E., Geer, K., Glill, R., Grady, M., Guerra, W., Gebregeorgis, E., Hawes, A., Henderson, N., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jang, H., Lews, A., Lewis, L., Koyar, C., Kowis, C., Kraft, C. L., Lebow, H., Lewan, J., Lewis, L., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J.,
                                                                                                                                                                                        ACU96698 145971 bp DNA 11near HTG 24-AUG-2002
Rattus norvegicus clone CH230-154C12, *** SEQUENCING IN PROGRESS
***, 68 unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Lorensuhewa, L., Loulseged, H., iozado, R.J., Lu, X., Ma, J.,
Maheshwari, M., Mahindartne, M., Martin, K., Martinez, E.,
Manguum, B., Mapua, P., Martin, K., Martinez, E.,
Mawhiney, S., Mcleod, M., Mcneill, T., Meenen, E., Milosavljeric, A.,
Minfa, E., Mnija, E., Montemayor, J., Moore, S., Morgan, M., Morris, K.,
Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D.,
Newton, N., Nguyen, N., Norris, S., Nwackelmeh, O., Okwuonu, G.,
Olarnpuusagoon, A., Pals, S., Parks, K., Pasternak, S., Paul, H.,
Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A.,
Perez, A., Regier, M.A., Reigh, R., Reilly, M., Rachlin, E.,
Reuves, K., Regier, M.A., Rigs, F., Rives, C., Rodkey, T., Rojas, A.,
Rose, M., Rose, K., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S.,
Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A.,
Stran, T., Sitter, C.D., Smajs, D., Sreed, A., Sodergren, E.,
Song, X.-Z., Sorelle, R., Sosa, J., Steinle, M., Strong, R.,
Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S.,
Tingey, A., Tabor, P., Wang, J., Wang, S., Warren, J.,
Wooden, H., Worley, K., Wijht, B., Wullson, R., Walker, B.,
Walker, B., Wang, J., Walker, S., Shuth, D., Rish, H.,
Wolley, R., Wijht, B., Wullson, R., Wulb, S.,
Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X.,
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NOTE: This is a 'working draft' sequence. It currently consists of 68 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-5FP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Sequencing vector: Plasmid;
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Sattus norvegicus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
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NOTE: This is a working draft' sequence. It currently consists of 68 contigs. The true order of the pieces is not known and their order in this sequence record is
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Rat Genome Sequencing Consortium.
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Submitted (24-AUG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Aug 14, 2002 this sequence version replaced gi:21735321.
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Contact: hgsc-help@bcm.tmc.edu
------- Project Information
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          MacDonald, M., Huckle, E., Wilkinson, P. and Micklem, G.
Direct Submission
Submitted (16-0CT-1995) The Sanger Centre, Hinxton, Cambridgeshire
CBIO 1RQ, England. E-mail contact: humquery@sanger.ac.uk
(bases 1 to 296)
Cross, S.H., Charlton, J.A., Nan, X. and Bird, A.P.
Purification of CpG islands using a methylated DNA binding column
Nat. Genet. 6 (3), 236-244 (1994)
94282070
                                                                                                                                               Clones are available from the UK MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridgeshire CB10 1RQ, UK. See URL: http://www.hgmp.nrc.ac.uk, for details or contact: biohelp@figmp.nrc.ac.uk.
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Pred. No. 5.6e-50;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="33f3"
/sex="male"
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/clone_lib="CGI-1"
/dev_stage="adult"
78 c 84 g
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Best Local Similarity 97.4%;
Matches 228; Conservative 0
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Matches 295; Conserv
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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July 18, 2003, 09:03:57; search time 0.492891 Seconds (without alignments) 673.193 Million cell updates/sec Run on:

US-09-857-308-5 37 1 LYQAVATI 8 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% -Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# STIMMARTES

	SUMMARII  ID  NORB_VIBAL  LPXK, HELPU  NORB_NEIMB  NORB_NEIMB  GAG_HVIRH  GITT_BACCA  GITT_BACCA  GITT_BACCA  GITT_BACCA  GITT_BACCA  GAG_HVIRH  GAG_HVIRH  GAG_HVIRH  GAG_HVIRH  EAA2_CAEEL  EAA2_MOUSE  EAA2_MOUSE  EAA2_MOUSE  EAA2_MOUSE  EAA2_MOUSE  EVGS_ECO5T  VCS3_YEACT  VCS3_YEACT  AMCL_ERWAM  NORB_VIBHA  OURZ_BOVIN  NIFE_SVNDW  NORB_VIBHA  EAA3_MOUSE  EAA3_MOU	DB 1D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Length DB ID 413 1 NOR 410 1 NOR 410 1 NOR 410 1 NOR 420 1 GAG 421 1 GLT 573 1 EAA 573 1 EVG 1197 1 EVG 1197 1 EVG 1197 1 LEVG 1197 1 LEVG 1197 1 GLT 483 1 UCR 469 1 UTF 523 1 GLT 560 1 GLT 575 1 GLT 575 1 GLT 575 1 OCR 575 1	DB 1D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Length DB ID 413 1 NOR 410 1 NOR 410 1 NOR 410 1 NOR 420 1 GAG 421 1 GLT 573 1 EAA 573 1 EVG 1197 1 EVG 1197 1 EVG 1197 1 LEVG 1197 1 LEVG 1197 1 GLT 483 1 UCR 469 1 UTF 523 1 GLT 560 1 GLT 575 1 GLT 575 1 GLT 575 1 OCR 575 1	SUMMARIES	scri	BAL 056587 vibrio alqí	Q9zmbl helicok		09k0m4	P05890	P24944	P24943	025605		010901	Q21353 caeno		P43006		P43004			057 P58402 escherichia			Q9ccs5	P45852	. 025095	046633	Q9rfw0	09kps2	P21345	P23004	1	0	E P51906 1	T 1007 234+110 2021
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P43005 homo sapien P31597 oryctolagus	Q04975 salmonella P10563 emericella	P03161 ground squi P97603 rattus norv	Q90610 gallus gall P23615 saccharomyc	Q92859 homo sapien P97798 mus musculu	Q66802 ebola virus Q90683 gallus gall	
EAA3_HUMAN EAA3_RABIT	VIPC_SALTI QUTA_EMENI	DPOL_HPBGS NEO1_RAT	NEO1_CHICK SPT6_YEAST	NEO1_HUMAN NEO1_MOUSE	RRPL_EBOSM ITF2_CHICK	
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75.7	75.7	75.7	75.7	75.7	75.7	
28 28	28 28	28 28	28 28	28 28	28 27	
3.4 3.5	36	38 30	40	42	44 45	

ALIGNMENTS	SU.		Na(+)-translocatin (Na(+)-translocati			-:		STRAIN-NCIMB 11038;		"Cloning and sequencing of four structural genes for the Na(+)-			SEQUENCE FROM N.A.	E (V)				quinone reductase from the marine Vibrio alginolyticus.";								MEDLINE=ZUUIDU49; FUDMEG=10349836; Nakayama Y., Hayashi M., Yoshikawa K., Mochida K., Unemoto T.;					COFACTOR, AND MASS SPECTROMETRY. MEDLINE=21099804; Pubmed=11163785;		"FMN is covarently attached to a threonine residue in the Ngrb and NgC subunits of Na(+)-translocating NADH-quinone reductase from	Vibrio alginolyticus.";
	N N N	1111	DE DE	DE GN	SO	38	R B	S S	RA RA	RT	R	A K	R.	R K	ZZ C	XX X	A E	RT	R R	RP	RX e	R.T.	RT	R R	RP	R X	RT	RT	R	RN	R R	RA	RT	X

312 AA

PRT;

STANDARD;

Created)

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-!- FUNCTION: TRANSFERS THE GAMMA-PHOSPHATE OF ATP TO THE 4'-POSITION OF A TETRAACYLDISACCHARIDE 1-PHOSPHATE INTERMEDIATE (TERMED DS-1-P) TO FORM TETRAACYLDISACCHARIDE 1,4'-BIS-PHOSPHATE (LIPID IVA)
                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-99120557; PubMed-9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Dolg P.C.,
Smith D.R., Noonan B., Gulla B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                        "Genomic sequence comparison of two unrelated isolates of the human
                                        16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tetraacyldisaccharide 4'-kinase (EC 2.7.1.130) (Lipid A 4'-kinase).
                                                                                                 Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
                                                                                                                                                                                                                                                                                          gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY).
                                                                                                                                           NCBI_TaxID=85963;
                                                                                       LPXK OR JHP031:
                           16-0CT-2001
                                                                                                                                                                                                                                                               Trust T.J.;
   LPXK_HELPJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NORB_NEIMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ÷
                                                                                                                                                                  "Na(+) translocation by bacterial NADH:quinone oxidoreductases: an extension to the complex-I family of primary redox pumps."; balohim. Biophys. Acta 1505:45-56(2001).

-! FUNCTION: NQR COMPLEX CATALYZES THE REDUCTION OF UBIQUINONE-I TO UBIQUINOL BY TWO SUCCESSIVE REACTIONS, COUPLED WITH THE TRANSPORT OF NA(+) IONS FROM THE CYTOPLASM TO THE PERIPLASM. NORA TO NQRE ARE PROBABLY INVOLVED IN THE SECOND STEP, THE CONVERSION OF UBISEMIQUINONE TO UBIQUINOL.
                                                                                                                                                                                                                                                                                                                                ENZYME REGULATION: THIS REACTION IS TIGHTLY COUPLED TO THE NA(+) PUMPING ACTIVITY AND SPECIFICALLY REQUIRES NA(+) FOR ACTIVITY. INHIBITED BY KORORMICIN AND 2-N-HEPTYL-4-HYDROXYQUINOLINE N-OXIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: COMPOSED OF SIX SUBUNITS; NORA, NORB, NORC, NORD, NORE
                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                       Hayashi M., Nakayama Y., Unemoto T.;
Recent progress in the Na(+) translocating NADH-quinone reductase
from the marine Vibrio alginolyticus.";
Biochim. Biophys. Acta 1505:37-44(2001).
                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+)(In) = NAD(+) + ubiquinol + Na(+)(Out).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB008030; BAA22911.1; -.
InterPro; IPR004338; NQR2_RnfD_RnfE.
Pfam; PF03116; NQR2_RnfD_RnfE; 1.
Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 1; Length 413; Pred. No. 4.2;
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-> G (IN REF. 1).
A6F849F7A5C91C9D CRC64;
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                                          MEDLINE-21145117; PubMed-11248187;
                                                                                                                                             MEDLINE=21145118; PubMed=11248188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
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75.0%;
 FEBS Lett. 488:5-8(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
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                                                                                                                                                           Steuber J.;
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                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Na(+)-translocating NADH-quinone reductase subunit B (EC 1.6.5.-)
(Na(+)-translocating NQR subunit B) (Na(+)-NQR subunit B) (NQR-1 subunit B) (NQR-1 subunit B).
CATALYTIC ACTIVITY: ATP + 2,3-bis(3-hydroxytetradecanoy1)-D-
glucosaniny1-(beta-D-1,6)-2,3-bis(3-hydroxytetradecanoy1)-D-
glucosaniny1 beta-phosphate = ADP + 2,3,2',3'-tetrakis(3-
hydroxytetradecanoy1)-D-glucosaniny1-1,6-beta-D-glucosanine 1,4'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE001467; AAD05884.1; -.
InterPro; IPR03758; LpxK.
InterPro; Doco666; LpxK; 1.
TIGRPAMS; TIGRO6682; Lipid A biosynthesis; Lipid synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43E44608F3A60FAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30; DB 1;
Pred. No. 16;
                                                                                                                    PATHWAY: Lipid A biosynthesis; sixth step. SIMILARITY: BELONGS TO THE LPXK FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           410 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding; Complete proteome. NP_BIND 60 67 ""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312 AA; 35567 MW;
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62.5%;
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Best Local Similarity
'-hoc 5; Conserva
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32 IYOCIATI 39
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                                                                                                  bisphosphate.
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õ g RESULT 2 LPXK\_HELPJ

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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
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                                              STRAIN=MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAG_HV1RH
P05890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26
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                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Na(+)-translocating NADH-quinone reductase subunit B (EC 1.6.5.-)
(Na(+)-translocating NQR subunit B) (Na(+)-NQR subunit B) (NQR-1 subunit B).
NQRB OR NMB0568.
                                                                                                                                                      "TET TO TO THE TRANSPORT OF THE REDUCTION OF UBIQUINONE-1 TO UBIQUINOL BY TWO SUCCESSIVE REACTIONS, COUPLED WITH THE TRANSPORT OF NA(+) IONS FROM THE CYTOPLASM TO THE PERIPPLASM. NORA TO NORE ARE PROBABLY INVOLVED IN THE SECOND STEP, THE CONVERSION OF UBISEMIQUINONE TO UBIQUINOL (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+)(In) = NAD(+) +
                                                     Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G., Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                            ubiquinol + Na(+)(Out).
COPACIOR: FWN (BY SIMILARITY).
SUBUNIT: COMPOSED OF SIX SUBUNITS; NQRA, NQRB, NQRC, NQRD, NQRE
AND NQRF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane; Inner membrane; Complete proteome.
80 POTENTIAL.
                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
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InterPro; IPR004338; NQP2_RnfD_RnfE.
Pfam; PF03116; NQP2_Rnf Briffs; 1.
Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4N (BY SIMILARITY).
D46528F211513ECE CRC64;
                                                                                                                                                                                                                                                                                    (Potential).
-!- SIMILARITY: BELONGS TO THE NORB/RNFD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              410 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                 STRAIN=22491 / Serogroup A / Serotype 4A; MEDLINE=20222556; PubMed=10761919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis (serogroup B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44536 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.18;
75.08;
                                                                                                                                    meningitidis 22491.";
Nature 404:502-506(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142
177
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341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            410 AA;
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                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Flavoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL outstation
                                                    MEDLINE=20175755; PubMed=10710307;
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Nelson W.C., Gwinn M.L., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Clecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.; Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -I- FUNCTION: NOR COMPLEX CATALYZES THE REDUCTION OF UBLQUINONE-1 TO UBLQUINOL BY TWO SUCCESSIVE REACTIONS, COUPLED WITH THE TRANSPORT OF NA(+) IONS FROM THE CYTOPLASM TO THE PERIPLASM. NORA TO NORE ARE PROBABLY INVOLVED IN THE SECOND STEP, THE CONVERSION OF UBISEMIQUINONE TO UBIQUINOL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+)(In) = NAD(+) + ubiquinol + Na(+)(Out).
COFACTOR: FWN (BY SIMILARITY).
SUBUNIT: COMPOSED OF SIX SUBUNITS; NQRA, NQRB, NQRC, NQRD, NQRE AND NORF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Flavoprotein; FMN; Transmembrane; Inner membrane; Complete proteome.
TRANSMEM 58 80 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
GAG polyprotein [Contains: Core proteins P17, P24, P2, P7, P1, P6].
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Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 30; DB 1; Length 410;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FMN (BY SIMILARITY).
F632E12206170B4F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR004338; NQR2_RnfD_RnfE.
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01-FEB-1994 (Rel. 28, Last sequ
15-JUN-2002 (Rel. 41, Last anno
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75.0%;
N.A.
Serogroup B;
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Matches 6; Conser
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GLTT_BACST
P24943;
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GLTT_BACST
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                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                        -i-FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROPEINS FORM MEMBRANE ASSCOLATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.

-i- PTM: THE P24 PROTEIN 1S PHOSPHORYLAND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Proton/sodlum-glutamate symport protein (Glutamate-aspartate carrier
protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
CORE PROTEIN P6.
CORE PROTEIN P6.
CCHC-TYPE I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORE PROTEIN P17 (MATRIX PROTEIN).
CORE PROTEIN P24 (CORE ANTIGEN).
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0
      Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11701;
                                                              Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C.,
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MYRISTATE (BY SIMILARITY).
44AA0CB5CDAEFF7B CRC64;
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                                                                                     Wong-Staal F.; Submitted (XXX-1987) to the HIV data bank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                  HSSP; P05888; 1AAF.
HIV; M17451; GAG$RF.
InterPro; IPR000721; Gag_p24.
InterPro; IPR000071; Retrovir_p17.
InterPro; IPR001878; Znf_CCHC.
                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00607; Gag_P24; 1.
PRINTS; PR00939; C2HCZNFINCER.
PRINTS; PR00234; HIVIMATRIX.
SMART; SM0043; ZnF_C2HC; 2.
PROSITE; PS50158; ZF_CCHC; 2.
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01-MAR-1992 (Rel. 21, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55825 MW;
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                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00098; zf-CCHC; 2.
Pfam; PF00540; Gag_p17; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
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77 LYNAVATL 84
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                                                  SEQUENCE FROM N.A.
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P24944;
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ZN_FING
LIPID
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GLTT_BACCA
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                            "Characterization and functional expression in Escherichia coli of the sodium/proton/glutamate symport proteins of Bacillus stearothermophilus and Bacillus caldotenax."; Mol. Microbiol. 6:2845-2856(1992).
-i- FUNCTION: THIS CARRIER PROTEIN IS PART OF THE NA(+)-DEPENDENT, BINDING-PROTEIN-INDEPENDENT GLUTAMMATE-ASPARTATE TRANSPORT SYSTEM.
                                                                                                                                                                                                                                                                                                                                        -:- SUBCELLULAR LOCATION: Integral membrane protein.
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01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Proton/sodium-glutamate symport protein (Glutamate-aspartate carrier
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Bacillus caldotenax.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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POTENTIAL.
EXTRACELLULAR (POTENTIAL).
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POTENTIAL.
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                                                                                                                                                    Tolner B., Poolman B., Konings W.N.;
"Characterization and functional expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
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1; Mismatches
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PROSITE; PSO0714; NA_DICARBOXYL_SYMP_2; 1.
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                                                                                                   SEQUENCE FROM N.A. MEDLINE-93062018; PubMed-1359385;
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75.08;
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Best Local Similarity 75.0
Matches 6; Conservative
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373
421 AA;
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                                                   NCBI_TaxID=1395;
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aspartate transporter)
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Q22682;
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                                                                             Tolner B., Poolman B., Konings W.N.;

"Characterization and functional expression in Escherichia coli of the sodium/proton/glutamate symport proteins of Bacillus stearothermophilus and Bacillus caldotenax.";

Mol. Microbiol. 6:2845-2856(1992).

-! FUNCTION: THIS CARRIER PROTEIN IS PARF OF THE NA(+)-DEPENDENT, BINDING-PROTEIN-INDEPENDENT GLUTAMATE-ASPRATATE TRANSPORT SYSTEM.
-! SUBCELLULAR LOCATION: Integral membrane protein.
-! SUBLIARITY: BELONGS TO THE SODIUM:DICARBOXXLATE SYMPORTER FAMILY
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Excitatory amino acid transporter (Sodium-dependent glutamate/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.4%; Score 29; DB 1; Length 421; 75.0%; Pred. No. 37; ive 1; Mismatches 1; Indels
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30C5738E8FD3A54F CRC64;
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                                                                                                                                                                                                                                                                                                                                              Transport; Transmembrane; Symport.
DOMAIN 1 3 CYTOPLASMIC (POTENTIAL).
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                   Firmicutes; Bacillales; Geobacillus.
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                                                                                                                                                                                                                                                                                                             Pfam; PF00375; SDF; 1.
PROSITE; PS00713; NA_DICARBOXYL_SYMP_1; 1.
PROSITE; PS00714; NA_DICARBOXYL_SYMP_2; 1.
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InterPro; IPR001991; Na/diCO_symp.
                                                           STRAIN=ATCC 7954;
MEDLINE=93062018; PubMed=1359385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45469 MW;
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         Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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169
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330
351
372
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                                                 SEQUENCE FROM N.A.
                             NCBI_TaxID=1422;
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Q25605;
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                    Bacteria;
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EAAT_ONCVO
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                                                                                                                  Gaps
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NCBI_TaxID=6239;
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15-JUN-2002 (Rel. 41, Last annotation update)
Putative sodium-dependent excitatory amino acid transporter T22E5.2.
              Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Onchocerca.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
CEE52D670F76A89E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane; Glycoprotein;
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InterPro; IPR001991; Na/dicO_symp.
Pfam; PF00375; SDF; 1.
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75.0%;
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67
105
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Onchocerca volvulus.
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                                                             NCBI_TaxID=6282;
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REVISIONS
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                                                                                                                                                                                                                                                                                      Pfam; PF00375; SUF; 1.

PRINTS; PR0173; EDTRNSPORT.

PROSITE; PS00713; NA_DICARBOXYL_SYMP_1; 1.

PROSITE; PS00714; NA_DICARBOXYL_SYMP_2; 1.

PROSITE; PS00714; Na_DICARBOXYL_SYMP_2; 1.

Hypothetical protein; Transport; Transmembrane; Glycoprotein; Symport.

Hypothetical protein; Transport; Croplasmic (Potential).
                                           Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: BELONGS TO THE SODIUM:DICARBOXYLATE SYMPORTER FAMILY
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Rhabd<u>itidae;</u> Peloderinae; Caenorhabditis.
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MEDLINE-97039669; PubMed-8885221;
Radice A.D., Lustigman S.;
Cloning and characterization of cDNAs encoding putative glutamate
transporters from Caenorhabbitis elegans and Onchocerca volvulus.";
Mol. Biochem. Parasitol. 80:41-53(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -LINKED (GLCNAC. . .) (POTENTIAL). 8B4C7469C594727D CRC64;
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010901; P90798; 017920;
01-NOV-1997 (Rel. 35, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2012 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
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WormPep; T22E5.2; CE04992.
InterPro; IPR001991; Na/diCO_Symp.
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Kawano T., Takuwa K., Nakajima T.;
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75.08;
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                                                                                          (SDF, TC 2.A.23)
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SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Bristol N2.

X MEDLINE-97321871; PubMed=9178573;

X MEDLINE-97321871; PubMed=9178573;

X Kawano T., Takuwa K., Nakajima T.;

T "Structure and activity of a new form of the glutamate transporter of the nematode Caenorhabditis elegans.";

Biosci. Biotechnol. Biochem. 61:927-929(1997).

- I- FUNCTION: TRANSPORTS L-GLITAMATE AND ALSO L- AND D-ASPARTATE.

ESSENTIAL FOR TERMINATING THE POSTSYNAPTIC ACTION OF GLUTAMATE BY RAPIDLY REMOVING RELEASED GLUTAMATE FROM THE SYNAPTIC CLEFT. ACTS

AS A SYMPORT BY CO-TRANSPORTING SODIUM (BY SIMILARITY).

- SUBCELLULAR LOCATION: Integral membrane protein.

- ALTERNATIVE PRODUCES 2 ISOFORMS; GLT-1 AND GLT-2 (SHOWN HERE);

ARE PRODUCED BY ALTERNATIVE SPLICING.

- SIMILARITY: BELONGS TO THE SODIUM:DICARBOXYLATE SYMPORTER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular cloning of a cDNA for the glutamate transporter of the nematode Caenorhabditis elegans."; Biochem. Biophys. Res. Commun. 228:415-420(1996).
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N-LINKED (GLCNAC. ..) (POTENTIAL).
MISSING (IN ISOFORM GLT-1).
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EXTRACELJULAR (POTENTIAL).
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                                                                                                                                                                     Nhan M., Hawkins J.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                  Waterston R.; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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ADTA -> ENTT (IN REF. 1).

A -> G (IN REF. 1).
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WormPep; C12012.2b; CE29084.
InterPro; IPR001991; Na/diCO_symp.
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EMBL; D86740; BAA13164.1; --
EMBL; U51998; AAL00857.1; --
EMBL; U51998; AAL00858.1; --
EMBL; D86741; BAA21840.1; --
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Created)
                                 15-JUN-2002 (Rel. 41,
Excitatory amino acid
SLCIA7 OR EAATS.
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560 AA;
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PRINTS; PR00173; EDTRNSPORT.

PROSITE; PS00713; Na_DICARBOXYL_SYMP_1; 1.

PROSITE; PS00714; Na_DICARBOXYL_SYMP_2; 1.

Hypothetical protein; Transport; Transmembrane; Glycoprotein; Symport.

5 CYTOPLASMIC (POTENTIAL).
                    Gaps
                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative sodium-dependent excitatory amino acid transporter KO8F4.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
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                   Indels
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Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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Pfam; PF00375; SDF; 1.
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WormPep; K08F4.4; CE06152.
75.0%;
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Best Local Similarity 75.0.
                 6; Conservative
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                                                                          366 LYEAVAAI 373
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532 AA;
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000341;
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Q21353;
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                                                                                                                                                                                                                                            -1- SUBUNIT: INTERACTS WITH THE PDZ DOMAINS OF DLG4.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- TISSUE SPECIFICITY: EXPRESSED PRIMARILY IN RETINA. DETECTABLE IN
LIVER, HERRY, MUSCLE AND BRAIN SOLIUM:DICARBOXYLATE SYMPORTER FAMILY
-1- SIMILARITY: BELONGS TO THE SODIUM:DICARBOXYLATE SYMPORTER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Last sequence update)
Last annotation update)
transporter 5 (Retinal glutamate transporter).
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DOMAIN 1 16 CYTOPLASMIC (POTENTIAL).
                                                                                                    Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -LINKEL (GLCNAC. . .) (POTENTIAL). C71D48355AACFF32 CRC64;
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PRINTS; PR00173; EDTRNSPORT.
PROSITE; PS00713; NA_DICARBOXYL_SYMP_1; 1.
PROSITE; PS00714; NA_DICARBOXYL_SYMP_2; 1.
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InterPro; IPR001991; Na/diCO_symp.
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P43006; 035877; 054686; 054687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60722 MW;
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75.0%;
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Genew; HGNC:10945; SLC1A7.
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U75373; AAB71738.1;

EMBL;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
STRAIN-JCL:ICR; TISSUE-Brain, and Liver;
MEDLINE-98039013; PubMed-9373176;
MEDLINE-98039013; PubMed-9373176;
M. Utsunomiya-Tate N., Endou H., Kanai Y.;
M. Utsunomiya-Tate N., Endou H., Kanai Y.;
M. Tissue specific variants of glutamate transporter GLT-1.";
FEBS Lett. 416:312-316(1997).
C. I- FUNCTION: TRANSPORTS L-GLUTAMATE AND ALSO L- AND D-ASPARTATE.
ESSENTIAL FOR TERMINATING THE POSTSYNAPTIC ACTION OF GLUTAMATE BY
RAPIDLY REMOVING RELEASED GLUTAMATE FROM THE SYNAPTIC CLEFT. ACTS
C. I- SUBCELLULAR LOCATION: Integral membrane protein.
C. I- ALTERNATIVE PRODUCTS: 3 ISOFORMS; GLT-1 (SHOWN HERE), GLT-1A
AND GLT-1B; ARE PRODUCED BY ALTERNATIVE SPLICING.
C. I- TISSUE SPECIFICITY: ISOFORM GLT1 IS EXPRESSED IN THE BRAIN.
C. I- FTM: GLYCOSYLATED.
C. I- FTM: GLYCOSYLATED.
C. I- STMILARTY: BELONGS TO THE SODIUM:DICARBOXYLATE SYMPORTER FAMILY
C. I- STMILARTY: BLONGS TO THE SODIUM:DICARBOXYLATE SYMPORTER FAMILY
                                                                                                                                                                                                                                                                                                                                                            STRAIN=JCL:ICR; TISSUB-Cerebellum;
MEDLINE-95284091; PubMed-7766664;
Mukainaka Y., Tanaka K., Hagiwara T., Wada K.;
"Molecular cloning of two glutamate transporter subtypes from mouse
                                                                                                                                                                                                                                                                   "Mouse excitatory amino acid transporter EAAT2: isolation, characterization, and proximity to neuroexcitability loci on mouse
                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-C57BL/6; TISSUE-Brain; MEDLINE-96032356; PubMed-7557442; Sutherland M.L., Delaney T.A., Noebels J.L.; "Molecular characterization of a high-affinity mouse glutamate
                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
MEDLINE=95213010; PubMed=7698742;
Kirschner M.A., Copeland N.G., Gilbert D.J., Jenkins N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peng J.-B., Guo L.-H.; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Excitatory amino acid transporter 2 (Sodium-dependent glutamate/aspartate transporter 2) (GLT-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                       Drain.;
Biochim. Biophys. Acta 1244:233-237(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U11763; AAA77673.1; -. EMBL; D43796; BAA07854.1; -. EMBL; U24699; AAA91643.1; -. EMBL; U75372; AAB71737.1; -.
                                                                                                                                                                                                                                                                                                             Senomics 24:218-224(1994).
                                                                                    SLC1A2 OR EAAT2 OR GLT1.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transporter.";
Gene 162:271-274(1995).
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                                                                                                                                                     NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                     chromosome
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
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Koepsell H., Storm-Mathisen J., Seeberg E., Kanner B.I.;
Nature 360:768-768(1992).
                                                                                         PRINTS; PR00173; EDTRNSPORT.
PROSITE; PS00713; NA_DICARBOXYL_SYMP_1; 1.
PROSITE; PS00714; NA_DICARBOXYL_SYMP_2; 1.
Transmembrane; Glycoprotein; Symport; Multigene family;
                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
MASTEG -> MVS (IN ISOFORMS GLT-1A AND ISOFORM GLT-1B).
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Pines G., Danbolt N.C., Bjoeraas M., Zhang Y., Bendahan A., Eide I
Koepsell H., Storm-Mathisen J., Seeberg E., Kanner B.I.;
"Cloning and expression of a rat brain L-glutamate transporter.";
Nature 360:464-467(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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G -> R (IN REF. 3).
A -> V (IN REF. 3).
T -> I (IN REF. 4).
K -> L (IN REF. 4).
K -> ED (IN REF. 3).
W, 13C7C3ODED4OCA81 CRC64;
                                                                                                                                                                                                                       POTENTIAL. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993 (Rel. 26, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Excitatory amino acid transporter 2 (Sodium-dependent Slutamate/Aspartate transporter 2) (GLUT-R) (GLT-1).
                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 29;
Pred. No.
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EMBL; AB007810; BAA23770.1; -. EMBL, AB007811; BAA23771.1; -. EMBL; AB007812; BAA23772.1; -. MGD; MGI:101931; Slcla2. InterPro: IPR001991; Na/diCO_symp.
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525
572
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                                                                              PF00375; SDF; 1
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525
572
572 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                               551
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P31596;
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                                                                                 Pfam;
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EAA2_RAT
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MUTAGEN
MUTAGEN
CONFLICT
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A REDLINE=94308247; PubMed=7913426.

Thistidine 326 is critical for the function of GLT-1, a (Na+ + K+)-
"Histidine 326 is critical for the function of GLT-1, a (Na+ + K+)-
"Histidine 326 is critical for the function of GLT-1, a (Na+ + K+)-
"Histidine 326 is critical from rat brain.";
J. Biol. Chem. 269:19573-19577(1994).

C. PUNCTION: TRANSPORTS L-GLUTAMATE AND ALSO L- AND D-ASPARTATE.

ESSENTIAL FOR TERMINATING THE POSTSYNAPTIC CLEFT. ACTS
C. AS SYMPORT BY CO-TRANSPORTING SODIUM.

C. I- SUBCELLIDIAR LOCATION: Integral membrane protein.

C. I- ALTERNATIVE PRODUCTS: 2 ISOPRAMS; GLT1 (SHOWN HERE) AND GLT-1A;
ARE PRODUCED BY ALTERNATIVE SPLICING.

C. I- ALTERNATIVE SPLICITY: LOCALIZED IN BRAIN AND IS HIGHLY ENRICHED IN
THE PURKINJE CELL LAYER IN CEREBELLUM.

C. I- PTW. GLYCOSYLATED.

C. I- PTW. GLYCOSYLATED.

SIMILARITY: BLONGS TO THE SODIUM:DICARBOXYLATE SYMPORTER FAMILY
                                                                                                                                                                                                                                                                                                                                                    "The rat hepatoma cell line H4-II-E-C3 expresses high activities of
the high-affinity glutamate transporter GLT-IA.";
FEBS Lett. 484:74-76(2000).
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PRINTS: PR00173; EDFRNSPORT.
PROSITE: PS00714; NA_DICARBOXIL_SYMP_1; 1.
PROSITE: PS00714; NA_DICARBOXIL_SYMP_2; 1.
Transport; Transmembrane; Glycoprotein; Symport; Multigene family;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
MASTEG -> MVS (IN ISOFORM GLT-1A).
KASTEG -> MVS (TRANSPORTER ACTIVITY.
                                                                                                                                                               TISSUE=Forebrain;
Roginski R.S., Choudhury K., Meiners S., Marone M., Basma A.N.,
                                                             Glutamate transporters from brain. A novel neurotransmitter
                                                                                                                                                                                                                              Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
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EMBL; U15098; AAA33061.1; -.
EMBL; U16098; AAA33062.1; ALT_INIT.
EMBL; AF297648; AAG13411.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                           MUTAGENESIS OF LYS-298 AND HIS-326.
                                                                                                                                                                                                                                                                                             TISSUE=Hepatoma;
MEDLINE=20521659; PubMed=11068035;
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                   MEDLINE-93292659; PubMed-8099882;
                                                                                     transporter family.";
FEBS Lett. 325:95-99(1993)
                                                                                                                                                                                                                                                                                                                                     Pollard M., McGivan J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SDF, TC 2.A.23).
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  REVISIONS TO 260-289
                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shimamoto K., Lebrun B., Yasuda-Kamatani Y., Sakaitani M., Shigeri Y., Yumoto N., Nakajima T.; "DL-thereo-b-benzyloxyaspartate, a potent blocker of excitatory amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --- FUNCTION: TRANSPORTS L-GLUTAMATE AND ALSO L- AND D-ASPARTATE. ESSENTIAL FOR TERMINATING THE POSTSYNAPTIC ACTION OF GLUTAMATE BY RAPIDLY REMOVING RELEASED GLUTAMATE FROM THE SYNAPTIC, CLEFT. ACTS
                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Pancreas;
MEDLINE-95002073; PubMed-7522567;
Manfras B.J., Rudert W.A., Trucco M., Boehm B.O.;
"Cloning and characterization of a glutamate transporter cDNA from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Brain;
MaDLINE=24227088; PubMed=8172925;
Shashidharan P., Wittenberg I., Plaitakis A.;
"Molecular cloning of human brain glutamate/aspartate transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
K->H,R: NORMAL TRANSPORTER ACTIVITY.
H->N,T,K,R: NO TRANSPORTER ACTIVITY.
V -> I (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain cortex;

MEDILINE=94365697; PubMed=7521911;

ARTIZA J.L., Fairman W.A., Wendy A., Wadiche J.I., Murdoch G.H.,

Kavanaugh M.P., Amara S.G.;

"Eunctional comparisons of three glutamate transporter subtypes
cloned from human mnotor cortex.";

J. Neurosci. 14:5559-5569(1994).
                                                                                                                                                                                                  ;
                                                                                                                                             DB 1; Length 573;
                                                                                                                                                                                                  1; Indels
                                                                                     8C51D30954E00E7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAA2_HUMAN STANDARD; PRT; 574 AA. P43004; 014417; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1995 (Rel. 34, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Excitatory amino acid transporter 2 (Sodium-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                       Pred. No. 51;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochim. Biophys. Acta 1191:393-396(1994).
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                                                                                                                                             Score 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glutamate/aspartate transporter 2)
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Mol. Pharmacol. 53:195-201(1998).
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298 K-326 H-521 V 62106 MW;
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                                                                                                                                          Similarity 75.0%; 6; Conservative
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298
326
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573 AA;
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                                                                                                                                                                       Local Similarity
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                                                                                        SEQUENCE
                                                                                                                                             Query Match
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us-09-857-308-5.rsp

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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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A -> S (IN REF. 2).
A -> G (IN REF. 3).
V -> E (IN REF. 3).
V -> E (IN REF. 1).
GIA -> AIP (IN REF. 3).
REMODENILMETWALLYIMIWYSP -> GQADGGFLQH
FERDCNEVSDHDHVVLS (IN REF. 3).
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InterPro: IPR001991; Na/diCO_symp.

Prom: PR00175; SDF: 1.

PROSITE; PR00173; Na_DICARBOXTL_SYMP_1; 1.

PROSITE; PS00714; Na_DICARBOXTL_SYMP_2; 1.

Transmembrane; Glycoprotein; Symport; Multigene family.

Transport; Transmembrane; Glycoprotein; Symport; Multigene family.

OYTOPLAGNIC (POTENTIAL).

A POTENTIAL.
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EXTRACELLULAR (POTENTIAL).
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POTENTIAL.
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Y -> F (IN REF. 3).
A -> G (IN REF. 3).
CSV -> RVL (IN REF. 3).
W -> G (IN REF. 3).
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N-LINKED (GLCNAC.
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Pred. No. 5
                                                                                                                                                                                                                                                                                                 POTENTIAL.
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                                                                      EMBL; U03505; AAA50429.1; -.
EMBL; U01824; AAA18900.1; -.
EMBL; 232517; CAA83532.1; -.
EMBL; D8584; BAA28706.1; -.
Genew; HGNC:10940; SLCIA2.
MIM; 600300; -.
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75.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
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Search completed: July 18, 2003, 09:57:52 Job time: 2.49289 secs

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Sequence 6, A Sequence 6, A Sequence 7, A Sequence 2, A Sequence 20, A Sequence 9, A Sequence 9, A

us-09-857-308-5.rai

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Sequence 81, Application US/09461697

Sequence 81, Application US/09461697

GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Donald C.
APPLICANT: Darney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT APPLICATION NUMBER: 1999-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND METHODS FOR DIAGNOSING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 37; DB 4; Length 363; Similarity 100.0%; Pred. No. 0.89; 8; Conservative 0; Mismatches 0; Indels
              US-09-368-282-6
US-09-56-708A-6
US-09-56-708A-7
US-08-529-654-2
US-09-042-709A-20
US-08-140-729A-9
US-08-140-729A-9
US-08-948-569A-6
US-08-663-808-8
US-08-663-808-8
US-09-042-950-9
US-09-042-960-9
US-09-042-960-9
US-09-133-740-8
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: COGENT NEUROSCIENCE, INC
APPLICANT: COGENT NEUROSCIENCE, INC
APPLICANT: Lo, Donald C.
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Furanam, Kasturi
APPLICANT: Ratz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS ANI
TITLE OF INVENTION: COMPOSITIONS ANI
TITLE OF INVENTION: CELL DEATH
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Patent No. 6277974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-461-697-81
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Best Local Similarity
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US-09-461-697-81
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US-09-461-697-77
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TYPE: PRT
SEQ ID NO 81
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330,
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Copyright (c) 1993 - 2003 Compugen Ltd
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US-08-695-301A-30
US-09-594-845-30
US-09-594-845-30
US-09-394-869-10
US-09-397-238A-10
US-09-397-238A-12
US-09-397-238A-12
US-09-397-238A-12
US-09-397-238A-12
US-09-1397-238A-12
US-09-1397-238A-17
US-08-146-745-7
US-08-166-7
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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37
1 LYQAVATI 8
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Maximum DB :
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STATE:
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                                                                                                                                                                                                                 100.0%; Score 37; DB 4; Length 412; 100.0%; Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: DANIEL H. ZIMMERWAN, PREM S. SARIN
TITLE OF INVENTION: Modified HGP-30 Peptides, Conjugates,
TITLE OF INVENTION: Compositions and Methods of Use
NUMBER OF SEQUENCES:
ADDRESSE: Law Office of Sherman and Shalloway
STREET: 413 N. Washington Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPOTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage
MEDIUM TYPE: 3.5 inch, 1.44 mb storage
COMPUTER: Dell System 210; Intel 80 286 Microprocessor
OPERATING SYSTEM: MS DOS 6.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.1%; Score 30; DB 3; Length 20; 75.0%; Pred. No. 1.3; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Word Perfect, Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/695,301A
FILING DATE: AUGUSt 9, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Richard A. Steinberg
REGISTRATION NUMBER: 26,588
REFERENCE/DOCKET NUMBER: 26,588
TELECOMMUNICATION INFORMATION:
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 77
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 30, Application US/08695301A Patent No. 6093400 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (703) 549-2282
TELEFAX: (703) 836-0106
INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
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STATE: Virginia
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TOPOLOGY: linear
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APPLICANT: DANIEL H. ZIMMERMAN, PREM S. SARIN
TITLE OF INVENTION: Modified HGP-30 Peptides, Conjugates,
TITLE OF INVENTION: Compositions and Methods of Use
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage MEDIUM TYPE: 3.5 inch, 1.44 mb storage COMPUTER: Dell System 210; Intel 80 286 Microprocessor OPERATING SYSTEM: MS DOS 6.22 SOFWWARE: Word Perfect, Version 5.1 CURRENT APPLICATION DATA:
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                                                                                                                 Modified HGP-30 Heteroconjugates, Compositions and Methods of Use
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OTHER INFORMATION: fragment of p-17 gag protein of
OTHER INFORMATION: HIV-IRF
                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Office of Sherman and Shalloway
STREET: 413 N. Washington Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Law Office of Sherman and Shalloway STREET: 413 N. Washington Street CITY: Alexandria
                                                                                      APPLICANT: DANIEL H. ZIMMERMAN, PREM S. SARIN TITLE OF INVENTION: Modified HGP-30 HeteroconfITLE OF INVENTION: Compositions and Methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.1%; Score 30; DB 75.0%; Pred. No. 1.3; ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/695,304C
FILING DATE: August 9, 1996
ATTORNEY AGENT INFORMATION:
NAME: RICHARD A Steinberg
REGIESTRATION NUMBER: 26,588
REFERENCE/DOCKET NUMBER: CELL-102
TELECOMMUNICATION INFORMATION:
TELEFORM
                   Sequence 30, Application US/08695304C Patent No. 6103239 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
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Best Local Similarity 75.0
Matches 6; Conservative
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                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                             STREET: 413 N Was
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
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US-08-695-304C-30
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APPLICANT: Amara, Jeffrey L
APPLICANT: Eliasof, Scott
APPLICANT: Eliasof, Michael P
APPLICANT: Exvanaugh, Michael P
TITLE OF INVENTION: Excitatory Amino Acid Transporter Genes
TITLE OF INVENTION: and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 560;
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ZURIE 60606
COMPUTER FEDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATEMIN PC-DOS/MS-DOS
SOFTWARE PATEMIN Release #1.0, Version #1.30
CURRENT APPLICATION NDATA:
APPLICATION NUMBER: 105/08/948,569A
FILING DATE: 10-CCT-1997
'ASSTRICATION: 435
                                                                                                                                                                            OTHER INFORMATION: fragment of p-17 gag protein of OTHER INFORMATION: HIV-1RF US-09-594-845-30
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Pred. No. 1.3;
1; Mismatches
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ATTORNEY/AGENT INFORMATION:
NAME: NO. 5882926nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,509-F
TELECOMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/08948569A Patent No. 5882926 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                          MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 10:
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Best Local Similarity 75.0%;
Matches 6; Conservative
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amino acid
  20 amino acids
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Matches 6; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                    NAME/KEY:
LOCATION: 75 to 94
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                         amino acid
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                                          TOPOLOGY:
  LENGTH:
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              MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage
MEDIUM TYPE: 3.5 inch, 1.44 mb storage
COMPUTER: 3.5 inch, 1.44 mb storage
COMPUTER: Dell System 210; Intel 80 286 Microprocessor
OPERATING SYSTEM: MS DOS 6.22
SOFTWARE: WORD Perfect, Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/589,768
FILING DATE: Concurrently herewith
ATTORIEY/AGENT INFORMATION:
NAME: Richard A. Steinberg
REGISTRATION NUMBER: 26,588
REGISTRATION NUMBER: 26,588
REGISTRATION NUMBER: CELL-101.01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHNORE: (703) 836-0106
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 omino acids
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ZIP: 22314
ZIP: 22314
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage
MEDIUM TYPE: 3.5 inch, 1.44 mb storage
COMPUTER: Dell System 210; Intel 80 286 Microprocessor
OPPERATING SYSTEM: MS DOS 6.22
SOFFWHARE: Word Perfect, Version 5.1
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APPLICANT: DANIEL H. ZIMMERNAN, PREM S. SARIN
TITLE OF INVENTION: Modified HGP-30 .Heteroconjugates,
TITLE OF INVENTION: Compositions and Methods of Use
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Office of Sherman and Shalloway
STREET: 413 N. Washington Street
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30; DB 4; Length 20; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 75 to 94
OTHER INFORMATION: fragment of p-17 gag protein of
OTHER INFORMATION: HIV-IRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Richard A. Steinberg
REGISTRATION NUMBER: 26,588
REFERENCE/DOCKET NUMBER: CELL-102.01
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/594,845
FILING DATE: CONCURRENTLY herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-594-845-30
; Sequence 30, Application US/09594845
; Patent No. 6287565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide FRAGMENT TYPE: internal fragment
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TELEFAX: (703) 836-0106
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
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75.0%;
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COMPUTER READABLE FORM:
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Best Local Similarity
Matches 6; Conserva
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TOPOLOGY: linear
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; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 10: US-09-397-238A-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/08948569A Patent No. 5882926 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 560 amino acids
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                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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Best Local Similarity 75.0
Matches 6; Conservative
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Patent No. 6284505
GENERAL INFORMATION:
APPLICANT: Amara, Susan G
Arriza, Jeffrey L
Ellasof, Scott
Kavanaugh, Michael P
TITLE OF INVENTION: Excitatory Amino Acid Transporter Genes and Uses
                                                                                                                                                                         APPLICANT: Kavanaugh, Michael P
TITLE OF INVENTION: Excitatory Amino Acid Transporter Genes
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 560;
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ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSE: McDonnell Boehnen Hulbert & Berghoff STRRET: 300 South Wacker Drive CIIY: Chicago STATE: 111inois COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/188,469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.4%; Score 29; DB 75.0%; Pred. No. 99; Live 1; Mismatches
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APPLICATION NUMBER: US/08/948,569
FILING DATE: 10-CCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: No. 5989825nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,509-F
                                        Sequence 10, Application US/09188469
Patent No. 5989825
GENERAL INFORMATION:
                                                                                                          APPLICANT: Amara, Susan G
APPLICANT: Arriza, Jeffrey L
APPLICANT: Eliasof, Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 10:
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 78.4
Best Local Similarity 75.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LYQAVATI 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                 90909
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RESULT 8
US-09-188-469-10
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Gaps
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APPLICANT: Arziza, Jeffrey L
APPLICANT: Eliasof, Scott
TITLE OF INVENTION: Excitatory Amino Acid Transporter Genes
TITLE OF INVENTION: and Uses
COMPUTER: FLORPY disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/397,238A

FILING DATA:

TELEPHONE: 312-913-0001

TELEPHONE: 312-913-0001

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 560;
99;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STAPE: 11linois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.4%; Score 29; DB 75.0%; Pred. No. 99; tive 1; Mismatches
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APPLICANT: Amara, Susan G
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                CITY: Chicago
                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 60606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens US-09-042-709A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LYQAVATI 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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LENGTH: 573
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APPLICANT: Arriza, Jeffrey L
APPLICANT: Eliasof, Scott
APPLICANT: Eliasof, Scott
TITLE OF INVENTION: Excitatory Amino Acid Transporter Genes
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
                                                                                     DB 2; Length 564; 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 564;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/09/188,469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.4%; Score 29; DB 2; 75.0%; Pred. No. 99;
                                                                                     Score 29; DB
Pred. No. 99;
1; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DIMBER:
10-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5998925ann, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,509-F
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 12, Application US/09397238A
; Patent No. 6284505
                                                                                                                                                                                                                                                                                Sequence 12, Application US/09188469
Patent No. 5989825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 12:
                                                                                   Query Match 78.4%;
Best Local Similarity 75.0%;
Matches 6; Conservative
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312-913-0002
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
              ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-948-569A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-188-469-12
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385 LYEAVAAI 392
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
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Gaps
                                                                      TITLE OF INVENTION: Excitatory Amino Acid Transporter Genes
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Pred. No. 99;
1; Mismatches 1; Indels
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                                                                                                                                                                ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION DATA: APPLICATION NUMBER: US/09/397,238A FILING DATE: 16-Sep-1999 CLASSIFICATION: VONKNOWN>
ATTORNEY AGENT INFORMATION: NUMBER: NO. 6284505nan, Kevin E REGISTRATION NUMBER: 35,303 REFERENCE/DOCKET NUMBER: 93,509-F TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: State of Oregon
APPLICANT: Amara, Susan G
APPLICANT: Amara, Jusffrey L
TITLE OF INVENTION: AMINO ACID TRANSPORTERS AND USES
FILE REFERENCE: 93.509-H (99/145)
CURRENT APPLICATION NUMBER: US/09/042,709A
CURRENT FILING DATE: 1998-03-17
PRIOR APPLICATION NUMBER: 140,729
PRIOR FILING DATE: 1993-10-20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 29; DB 4;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-397-238A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19, Application US/09042709A Patent No. 6458571
                                               Kavanaugh, Michael
Arriza, Jeffrey L
Eliasof, Scott
                                                                                          and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 564 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.4%;
75.0%;
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SEQUENCE CHARACTERISTICS
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75.0%;
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                                                                                                                   NUMBER OF SEQUENCES: 10
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Search completed: July 18, 2003, 10:01:23 Job time: 1.60664 secs
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                                                                                                                                                Sequence 7, Application US/08140729A
| Patent No. 5568782
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Arriza, Jeffrey L
| TITLE OF INVENTION: Amino Acid Transporters and Uses:
| NUMBER OF SEQUENCES: 17
| CORRESPONDENCE ADDRESS:
| ADDRESSE: Allegretti & Witcoff, Ltd.
| STREET: 10 South Wacker Drive, Suite 3000
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
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ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/140,729A
TI,ING DATE: 20 OCT 1993
TI,ING DATE: ANTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/08546666
Patent No. 5776774
GENERAL INFORMATION.
APPLICANT: Amara, Jeffrey L
TITLE OF INVENTION: Amino Acid Transporters and Uses
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
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1e+02;
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STREET: 10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 29; DB 1
Pred. No. 1e+02
1; Mismatches
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: NO. 5658782780n, Kevin E
REGISTRATION NUMBER: 35,309
REFERENCE/DOCKET NUMBER: 93,509
TELEPHONE: 312-715-1000
TELEPHONE: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 7:
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Best Local Similarity 75.0%;
Matches 6; Conservative
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amino acid
6; Conservative
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                                                      ||:||| |
403 LYEAVAAI 410
                                   1 LYQAVATI 8
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                                                                                                                                   US-08-140-729A-7
                                                                                                                                                                                                                                                                                                                                       STATE: I
COUNTRY:
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                         E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 29; DB 1
Pred No. 1e+02
1; Mismatches
                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/546,666
FILING DATE:
CLASSIFICATION NUMBER: US 08/140,729
FILING DATE:
APPLICATION NUMBER: US 08/140,729
FILING DATE: 20 OCT 1993
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5776774 nam. Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 35,303
TELECOMMUICATION INFORMATION:
TELECHONE: 312-715-1000
TELEFAX: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.4%;
75.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-546-666-7
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||:||| |
403 LYEAVAAI 410
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9526, Ap 13865, A 7860, Ap 349, App 905, App 955, App 9, Appli

678, App 977, App 12625, A 6050, Ap 323, App 546, App 323, App 364, App

Sequence 9 Sequence 10 Sequence 2 Sequence 3 Sequence 3

56, Appl 13419, A

2, Appli 4, Appli 1, Appli 1, Appli 3, Appli 85, Appli 2, Appli

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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APPLICANT: COGENT MECROSCIENCE, Inc.
APPLICANT: COGENT MECROSCIENCE, Inc.
APPLICANT: Lo. Donald C.
APPLICANT: Barney, Shart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Promain, Masturi
APPLICANT: Promain, Masturi
APPLICANT: Promain, Masturi
APPLICANT: Portbury, Stuart D.
APPLICANT: Promain, Masturi
APPLICANT: Ratz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-99
CURRENT APPLICATION NUMBER: US/09/9122,261
CURRENT FILING DATE: 2001-08-03
PRIOR FILING DATE: 1991-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 37; DB 11; Length 363; 100.0%; Pred. No. 3; ive 0; Mismatches 0; Indels
                      US-10-156-761-13865
US-10-156-761-13865
US-10-156-761-13865
US-10-101-464A-955
US-10-101-464A-955
US-10-101-464A-955
US-10-261-399-9
US-10-261-399-9
US-10-101-464A-977
US-10-101-464A-977
US-10-101-126-50
US-10-101-126-50
US-10-103-313-364
US-10-103-313-364
US-10-103-313-364
US-10-103-313-364
US-10-103-313-364
US-10-103-313-364
US-10-103-313-364
US-10-104-4-4
US-09-912-787-85
US-09-772-116-1
US-09-912-787-85
                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 81, Application US/09922261 Patent No. US20020111471A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      11
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Best Local Similarity 100.
Matches 8; Conservative
; ORGANISM: Homo sapiens US-09-922-261-81
 SEQ ID NO 81
LENGTH: 363
TYPE: PRT
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                                                                                           July 18, 2003, 09:57:18; Search time 1.1564 Seconds (without alignments) 821.584 Million cell updates/sec
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Sequence 77,
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Sequence 56,
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Sequence 56,
Sequence 24,
Sequence 24,
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                                                                                                                                                                                                                                                                                                                                                                                                                           (egn2_6/ptodata/2/pubpaa/US07_NEW_DUB.pep:*
(cgn2_6/ptodata/2/pubpaa/US07_NEW_DUB.pep:*
(cgn2_6/ptodata/2/pubpaa/US06_NEW_DUB.pep:*
(cgn2_6/ptodata/2/pubpaa/US06_NEW_DUB.pep:*
(cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
(cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
(cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
(cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
(cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
(cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
(cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
(cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
(cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
(cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
(cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
(cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
(cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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/cgn2_6/ptodata/A/pubpaa/US10_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-043-487-287
US-10-043-487-287
US-10-034-623-56
US-10-027-801-56
US-10-027-801-24
US-10-034-623-24
US-10-027-801-24
US-10-027-801-24
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                                                                                                                                                                                                                                                      451899 seqs, 118759770 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                 Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                  - protein search, using sw model
                                                                                                                                                                                                                          Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                              seq length: 0
seq length: 200000000
                                                                                                                                               US-09-857-308-5
37
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Match 1
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100.0
94.6
86.5
86.5
883.8
83.8
83.8
83.8
78.4
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Gaps

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446, App 70, Appl

440,

Sequence Seq

US-10-261-399-7 US-09-759-130B-440 US-09-759-130B-446 US-10-042-431-70

US-09-748-657-2 US-09-040-736-2

229 229 229 229 229 229 239 239

Result

APPLICANT: APPLICANT:

TYPE: PRT

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                    TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM FILE REFERENCE: DOORP.002A
CURRENT APPLICATION NUMBER: US/10/027,806
CURRENT FILING DATE: 2001-12-21
PRIOR PILLING DATE: BARLIER RPPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 56
LENGTH: 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Feldman, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
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APPLICANT: Schleper, Christa
TILLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/10/027,801
CURRENT PILING DATE: 2001-12-13
PRIOR PILING DATE: EARLIER PILING DATE: 1999-09-29
NUMBER OF SEO ID NOS: 123
SOFTWARE: PASTSEQ for Windows Version 3.0
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Pred. No. 27;
0; Mismatches
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CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 56
LENGTH: 273
                                                                                                                                                                                                                                                                                                                                   Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 56, Application US/10034623
Publication No. US20020198355A1
GRERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
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                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-027-806-56
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US-10-034-623-56
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87.5%;
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Best Local Similarity 87.5%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 87.5
Matches 7; Conservative
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178 LYQAVPTI 185
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US-10-034-623-56
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TITLE OF INVENTION: Protein interactions between Shigella Flexneri polypeptid
TITLE OF INVENTION: mammalian polypeptides
FILE REFERENCE: B4778A
CURRENT APPLICATION NUMBER: US/10/043,487
CURRENT FILING DATE: 2002-04-30
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 561
SOFTWARE: PATENTIN version 3.1
                                                                                                                                                                                            APPLICANT: Katz, Lawrence C.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CORRENT APPLICATION NUMBER: US/09/922,261
PRIOR APPLICATION NUMBER: US/09/461,697
PRIOR FILING DATE: 1999-12-14
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 287, Application US/10043487
Publication No. US20030055220A1
GENERAL INFORMATION:
APPLICANT: HYBRIGENICS
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                                                                    APPLICANT: COGENT NEUROSCIENCE, Inc
Sequence 77, Application US/09922261 Patent No. US20020111471A1 GENERAL INFORMATION:
                                                                                                          Barney, Shawn
Thomas, Mary Beth
Portbury, Stuart D.
Puranam, Kasturi
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; ORGANISM: Shigella Flexneri
US-10-043-487-287
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Best Local Similarity 100.
Matches 8; Conservative
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Matches 6; Conservative
                                                                                        Lo, Donald C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-922-261-77
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770 LYQAIATV 777
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US-10-027-806-56
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ENGTH: 897
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APPLICANT:
APPLICANT:
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Query Match

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Sequence 8, Application US/09815923
Sequence 8, Application US/09815923
Publication No. US200201976441
GENERAL INFORMATION:
BAPLICANT: Gill, Sarjeet S.
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of Insect Cell Membrane Transporters as No. US20020197644A
TITLE OF INVENTION: Target Sites for Insecticides
FILE REFERENCE: 023070-093800US
CURRENT APPLICATION NUMBER: US/09/815,923
CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
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                                                                                                                                                                                                                          APPLICANT: Swanson, Ronald V. APPLICANT: Swanson, Robert A. APPLICANT: Scanson, Robert A. APPLICANT: Scanson, Robert A. APPLICANT: Schleper, Christa TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM FILE REFERENCE: DCORP.002A CURRENT APPLICATION NUMBER: US/10/027,801 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: EARLIER APPLICATION NUMBER: EARLIER FILING DATE: 1999-09-29 SOFTWARE: FRSESO for Windows Version 3.0 SOFTWARE: PRASESO for Windows Version 3.0
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Pred. No. 44;
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                                                                                                                                                                  ; Sequence 24, Application US/10027801; Publication No. US20030054364A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Cenarchaeum symbiosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.8%;
75.0%;
                                                                                                                                                                                     Publication No. US20030054364A1
GENERAL INFORMATION:
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Matches 6; Conservative
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174 LYQAVPTV 181
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Best Local Similarity
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APPLICANT: Swanson, Ronald V.
APPLICANT: Feldman, Robert A.
APPLICANT: Feldman, Robert A.
APPLICANT: Feldman, Robert A.
APPLICANT: Feldman, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REPERENCE: DOORP.002A
CURRENT APPLICATION NUMBER: US/10/027,806
CURRENT FILING DATE: Z001-12-21
PRIOR PPLICATION NUMBER: EARLIER PPLICATION NUMBER: 09/408,020
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
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Sequence 24, Application US/10034623

Fublication No. US20020198365A1

SEQUENCE A. Manson, No. US20020198365A1

SERENAL INFORMATION:
APPLICANT: Swanson, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCORP.002A

CURRENT APPLICATION NUMBER: US/10/034,623

CURRENT PILING DATE: 2001-12-21

PRIOR FILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-09-29
                                                                                                                                                                      Gaps
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Pred. No. 44;
1; Mismatches 1; Indels
                                                                                                                         Length 273;
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Pred. No. 44;
1; Mismatches · 1; Indels
                                                                                                                                                                      1; Indels
                                                                                                                         DB 15;
27;
                                                                                                                         Score 32; DB 1
Pred. No. 27;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/102,294
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 24
LENGTH: 269
                                                                                                                                                                                                                                                                                                            RESULT 7
US-10-027-806-24
; Sequence 24, Application US/10027806
; Publication No. US20020160476A1
                                         ; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-027-801-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Cenarchaeum symbiosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Cenarchaeum symbiosum
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75.0%;
                                                                                                                      Query Match 86.5%;
Best Local Similarity 87.5%;
Matches 7; Conservative
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                                                                                                                                                                                                                                         178 LYQAVPTI 185
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Best Local Similarity
6; Conservat
                                                                                                                                                                                                           1 LYQAVATI 8
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Best Local Similarity
Matches 6; Conserv
; SEQ ID NO 56
; LENGTH: 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 269
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ZIP: 60606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                     US-10-261-399-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                     RESULT 13
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                                                                                                                                                                                                                                                      Length 574;
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Pred. No. 2.7e+02;
1; Mismatches 1; Indels
GENERAL INFORMATION:
APPLICANT: HEYWOOD, JAMES
TITLE OF INVENTION:
FILE REFERENCE: 102243-8
CURRENT FILING DATE: 2000-12-22
PRIOR PAPLICATION NUMBER: 60/173,764
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 2
LENGTH: 574
                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09040736
Publication No. US20030060617A1
GENERAL INFORMATION:
APPLICANT: Lin, Chieng-Liang Glenn
APPLICANT: Bristol, Lynn A.
TITLE OF INVENTION: DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,736
FILING DATE: 18-MAR-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                      Score 29; DB 10;
Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Corless, Peter F. REGISTRATION NUMBER: 33,860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                    78.4%;
75.0%;
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75.0%;
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amino acid
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Best Local Similarity 75.0°
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Best Local Similarity 75.0.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-040-736-2
                                                                                                                                                                                                                                                                                                                                        403 LYEAVAAI 410
                                                                                                                                                                                                         ORGANISM: Homo sapiens
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403 LYEAVAAI 410
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                                                                                                                                                                                                                                                                                                                     1 LYQAVATI 8
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                                                                                                                                                                                                                       US-09-748-657-2
                                                                                                                                                                                                                                                                                                                                                                                                            US-09-040-736-2
                                                                                                                                                                                         TYPE: PRT
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Gaps
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                                                                  Arriza, Jeffrey L
TITLE OF INVENTION: Amino Acid Transporters and Uses
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                  ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/140,729
FILING DATE: 20 OCT 1993
ATTORNEY/AGENT INFORMATION:
NAME: NO. US20030125538Alnan, Kevin E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 29; DB 15;
Pred. No. 2.7e+02;
1; Mismatches 1
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REFERENCE/DOCKET NUMBER: 93,509
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-261-399-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 440, Application US/09759130B Publication No. US20030022279A1
Sequence 7, Application US/10261399
Publication No. US20030125538A1
GENERAL INFORMATION:
APPLICANT: Amara, Susan G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
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Fraser, Christopher C
Sharp, John D
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75.0%;
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Kirst, Susan J
Mackay, Charles R
Myers, Paul S
Leiby, Kevin R
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 78.4
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                CITY: Chicago
STATE: IL
                                                                                                                                                                                                                     COUNTRY: USA
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Score 29; DB 12; Length 760;
Pred. No. 3.6e+02;
0; Mismatches 1; Indels
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 09/596,194
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 460
SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 446
LENGTH: 760
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Mus sp. US-09-759-130B-446
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APPLICANT: Sharp, John D
APPLICANT: Sharp, John D
APPLICANT: Barnes S
APPLICANT: Barnes S
APPLICANT: Mackay, Charles R
APPLICANT: Mackay, Charles R
APPLICANT: Myers, Paul S
APPLICANT: Myers, Paul S
APPLICANT: Goodearl, Andrew
APPLICANT: Goodearl, Andrew
APPLICANT: Holtzman, Douglas A
APPLICANT: Holtzman, Douglas A
APPLICANT: Holtzman, Douglas A
APPLICANT: Holtzman, Uses.
TITLE OF INVENTION: PROSOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: WESS.
     TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
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Pred. No. 3.6e+02;
0; Mismatches 1; Indels
                                                                      TITLE DEFENDENTION:
CURRENT APPLICATION NUMBER: US/09/759,130B
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 09/479,249
PRIOR FILING DATE: 2000-01-07
PRIOR RELING DATE: 2000-01-07
PRIOR RELING DATE: 2000-04-27
PRIOR PILING DATE: 2000-05-24
PRIOR PRILING DATE: 1909-06-14
PRIOR PRILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
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CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 09/479,249
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/559,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-06-30
PRIOR PELLING DATE: 2000-06-30
PRIOR PELLING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR FILING DATE: 1999-10-19
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PRIOR APPLICATION NUMBER: US 09/578,063
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APPLICATION NUMBER: US 09/333,159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 446, Application US/09759130B Publication No. US20030022279A1 GENERAL INFORMATION:
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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620 LYQCVAT 626
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; ORGANISM: Mus sp.
US-09-759-130B-440
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July 18, 2003, 07:41:22; Search time 399 Seconds (without alignments) 8846.602 Million cell updates/sec
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7: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/ptodata/2/pubpna/US09\_NEW\_PUB.seq3:\*/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*

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/cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\* /cgn2\_6/ptodata/2/pubpna/USS10\_PUBCOMB.seq:\* /cgn2\_6/ptodata/2/pubpna/USS0\_NEW\_PUB.seq:\* /cgn2\_6/ptodata/2/pubpna/USS0\_PUBCOMB.seq:\*

	Description	Sequence 75, Appl	76,		92,		1473	Sequence 36873, A			352,	٠,	3654,	٠,	94,	112	114,
SUMMARIES	ΩI	US-09-922-261-75	US-09-922-261-76	us-09-922-261-80	US-09-922-261-92	US-09-922-261-96	US-09-918-995-14733	US-09-918-995-36873	US-09-918-995-31390	US-09-922-261-100	US-09-764-847-352	US-10-092-154-352	US-09-918-995-3654	US-09-922-261-104	US-09-922-261-94	US-09-922-261-112	US-09-922-261-114
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Sequence 3427, Ap Sequence 78, Appl Sequence 88, Appl Sequence 116, App Sequence 90, Appl		Sequence 8022, App Sequence 8022, Ap Sequence 2124, Ap Sequence 635, App Sequence 11, Appl Sequence 27, Appl Sequence 88, Appl	
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## ALIGNMENTS

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464 CCCTCAGCCAACAAGCCCCCCCCTATGCTGGACATCCCCTCAGAGCCATGTAGT 523	584 ACAGCTCAGGACCAGAACAGCAGACAGAGGTGTAAAACTGAAGAGTGAACCT 643	704         AATCCCAATGCACATTCCAGATCCGGCACAGTGACCCAGAGAGTGACTTTTATCGTGGG .763           111111111111111111111111111111111111	### ##################################	GACCGGGAGGCCCGGCTGGGACTCCTTTTCCTGATGTGATGGAGCAGGTATTCCAT	1004 TATCACAGITACCAGATATACCAGAGATTCIGGAGATACCACACACACACATAGAC 1003		1184 GACATCACTTTCCTGTCAGTGAGGAGCTGGAGCTGACCTTGGTTCTGGAGACCAGTCA 1243 	1244 CTGCCTATGGGAGTGCTTGGGGCTCAGAGCGAACGCTTCCCATCTAACCTGGAGGTTGAA 1303	1304 GCTTCACCACAGGCTTCAAGTGCAAAATGCTTCTCCTCTTTGGAATCTGGCCCAT 1363 	1364 GTGAAAATGGAGCCTCAAGAAAGTGAAGAAGGCAATGTCTCTGGGCATGGTGTGCTGGGC 1423 	1424 AGTGATGTCTTCGAGGAGCCTATGTCAGGCATGAGTGAAGCTGGGATTCCTCAGAGCCCT 1483	1484 GATGACTCAGATAGCAGCTATGGTTCCCACTCACAGCGTCCTCATGGGGTCCTCCCCT 1543 

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APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Katz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CALL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/922,261
CURRENT FILING DATE: 1999-12-14
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APPLICANT: COGENT NEUROSCIENCE, INC
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	RESULT 5 US-09-922-261-96 Sequence 96, Application US/0992261 Sequence 96, Application US/0992261 Sequence 96, Application US/0992261 Sequence 96, Application US/0992261 Septent No. US20020111471a1 Septent No. US20020111471a1 Septicant: Loop Lonald C. APPLICANT: Loop Lonald C. APPLICANT: Porthury, Shawn APPLICANT: Puranam, Kasturi D. APPLICANT: Puranam, Kasturi D. APPLICANT: Ratz, Lawrence C. TITLE OF INVENTION: CELL DEATH STILE REFERENCE: 10001-005-99 CURRENT APPLICATION NUMBER: US/09/922,261 CURRENT APPLICATION NUMBER: US/09/461,697 PRIOR APPLICATION NUMBER: US/09/461,697 PRIOR PILING DATE: 1999-12-14 NUMBER OF SEQ ID NOS: 466 SEQ ID NO 96 LENGTH: 510 TYPE: DNA CORCANISM: Homo sapiens US-09-922-261-96	Query Match 29.8%; Score 510; DB 11; Length 510; Best Local Similarity 100.0%; Pred. No. 4.5e-140; Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps	DD 1076 ATGCTACAGATTAGTAAGCAACTCTCTGAAGAATATGAAAGGATTGTCAATCCTGAGAAG	Qy 1136 GCCACAGAGGACGCTAAACCTGTGAAGATCAAGGAGGAACCTGTGAGCGACATCACTTT	9y 1196 CCTGTCAGTGAGGAGCTGGAGCTGACCTTGCTTCTGGAGACCAGTCACTGCTATGGGA	Qy 1256 GTGCTTGGGGCTCAGAGCGAACGCTTCCCATCTAACCTGGAGGTTGAAGCTTCACCACAGG	Oy 1316 GCTTCAAGTGCAGAGGTAAATGCTTCTCCTCTTTGGAATCTGGCCCATGTGAAAATGGAG DY 241 GCTTCAAGTGCAAGGTAAATGCTTCTCCTCTTTGGAATCTGGCCCATGTGAAAATGCAGAGGTAAATGCTTCTCCTCTTTGGAATCTGGCCCATGTGAAAATGCAGAGGTAAATGCTTCTCCTCTTTGGAATCTGGCCCATGTGAAAATGCAGA	Qy 1376 CCTCAAGAAAGTGAAGAAGGCAATGTCTCTGGGCATGTGTGTG	1436
	RESULT 4  US-09-922-261-92  Sequence 92, Application US/0992261  Patent No. US20020111471A1  GENERAL INFORMATION:  APPLICANT: COGENT NEUROSCIENCE, Inc.  APPLICANT: COGENT NEUROSCIENCE, Inc.  APPLICANT: Thomas, Mary Beth  APPLICANT: Puranam, Kasturi  APPLICANT: Puranam, Kasturi  APPLICANT: Puranam, Kasturi  APPLICANT: Puranam, Kasturi  APPLICANT: Puranam, Cacle Darth  APPLICANT: Puranam, Cacle Darth  APPLICANT: COMPOSITIONS OND METHODS FOR DIAGNOSING  APPLICANT: Ratz, Lawrence C.  TITLE OF INVENTION: CACLE DATH  TITLE OF INVENTION: CACLE DEATH  TITLE OF INVENTION WINBER: US/09/922,261  CURRENT APPLICANTON NUMBER: US/09/461,697  PRIOR PRILING DATE: 1999-12-14  NUMBER OF SEQ ID NOS: 466  SEQ ID NO 92  LENGTH: 600  TTYPE: DNA  TYPE: DNA  TYPE: DNA  CORGANISM: HOMO SapienS	Ouery Match 35.1%; Score 600; DB 11; Length 600; Best Local Similarity 100.0%; Pred. No. 1.2e-166; Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	OY 986 AIGGAGCAGGTATICCATGAAGTGGGTATIGGCAGTGTGCTCTCCCTCCAGAGTTCTGG 1045	QY 1046 CAGCACCGCATCAAGACTATCACAGTTACATGAGATTAGTAAGCAACTCTCTGAA 1105	OY 1106 GAATATGAAAGGATTGTCAATCCTGAGAGGCCACAGAGGACGCTAAACCTGTGAAGATC 1165	Qy         1166 AAGGAGCAACCTGTGAGGGACTTGTCAGTGAGGGCTGAGCTT 1225           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY 1226 GCTTCTGGAGACCAGTCACTGCCTATGGGAGTGCTTGGGGCTCAGAGCGAACGCTTCCCA 1285	Qy         1286 TCTAACCTGGAGGTTGAAGCTTCACCACAGGCTTCAAGTGCAGAGGTAAATGCTTCTCCT 1345           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	CTCT

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1519 TGACAGCCTCATGGGGTCCTCCCCTGTTT 1547
                                                                                               ; Sequence 36873, Application US/09918995; Publication No. US20030073623A1; GENERAL INFORMATION:
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99.2%;
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Best Local Similarity 99.2'
Matches 376; Conservative
                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 38054
                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-918-995-36873
                                                                                  US-09-918-995-36873
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                                                                                                                                                                                                                                                                                           LENGTH: 379
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 2011-756
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/215,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14733
LENGTH: 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 29.6%; Score 505.8; DB 12; Length Best Local Similarity 99.6%; Pred. No. 8.4e-139; Matches 507; Conservative 0; Mismatches 2; Indels
                                                                                           Sequence 14733, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: misc_feature
; LOCATION: (1)...(573)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-14733
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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1038 AGTICTGGCAGCACCGCATCAAGGACTATCACAGTTACATGCTACAGATTAGTAAGCAAC 1097
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Pred. No. 5.1e-100;
0; Mismatches 3; Indels 0;
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; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq. Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
; TITLE OF INVENTION: ROWHER: US/09/918,995
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR FILING DATE: 1999-01.20
; NUMBER OF SEQ ID NOS: 38054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION OF THE COURT OF THE
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TCAGATAGCAGCTATGGTTCCCACTCCACTGACAGCCTCATGGGGTCCTCCCCTGTTTTC 1549
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                                                                                                                                                                                                                                            1250 ATGGGAGTGCTTGGGGCTCAGAGCGAACGCTTCCCATCTAACCTGGAGGTTGAAGCTTCA
                                                                                                                                                          1 ATGGGAGTGCTTGGGGCTCAGAGCGATCCCATCTAACCTGGAGGTTGAAGCTTCA
                                                                                                                                                                                                                   1310 CCACAGGCTTCAAGTGCAGAGGTAAATGCTTCTCCTCTTTGGAATCTGGCCCATGTGAAA
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                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVESTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 2003
SOFTWARE: Patentin Ver. 2.0
                                                  Indels
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                         Pred. No. 9.3e-89;
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                                                     Mismatches
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; OTHER INFORMATION: n equals a,t,g, or C
US-09-764-847-352
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100.08; Pre-
                                                  Matches 336; Conservative
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Matches 321; Conservative
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                         Best Local Similarity
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OTHER INFORMATION:
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OTHER INFORMATION:
NAME/KEY: SITE
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LENGTH: 517
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APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Puranam, Kasturi
APPLICANT: CALL DEATH
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CELL DEATH
FILE O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 ACGCGAGCCTTGCCTCAGGCCTCTCGAGGTCCAGACTGCCGCCCAGTCCGCTCTGCGACG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCTGCCCTGAACGTCAGGCGACCTCAGGACCCTGTGATTGGCGCCTGCGCCGGCGGCCGACC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ACGCGATCCTTGCCTCAGGCCTCTCGAGGTCCAGACAGCCGCCCAGCCCGCTCTGCGACG
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                                                                                                                                                                                                                                                                                                                        Length 491;
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                                                                                                                                                                                                                                                                                                                           Score 337; DB 12;
Pred. No. 5.9e-89;
                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                   SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 31390
LENGTH: 491
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APPLICANT: COGENT NEUROSCIENCE, INC
                                                                                                                                                                                 ; NAME/KEY: misc_feature
; LCCATION: (1)...(491)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31300
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 95.8%;
Matches 346; Conservative
                                                                                                                              ORGANISM: Homo sapiens
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US-09-922-261-100
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US-09-922-261-100
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Sequence 3654, Application US/09918995
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US-09-918-995-3654
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LENGTH: 216
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AGGGACTTGGGCATTCCTTGGGCTCCGTGCCTGTTCTTCGTGCTCCTTTCGGGCAAGGAT 260
                                                       AGGGACTTGGGCATTCCTTGGGCTCCGTGCCTGTTCTTCGTGCTCCTTTCGGGCAAGGAT 260
                                                                      CCTCCTTGTCTCGGTTCAGGTCCAGACCTCCCCGTCTTCCGGCTGCCCTGAACGTCAGGC 140
                         195 AGGGACTTGGGCATTCCTTGGGCTCCGTGCCTGTTCTTCGTGCTCCTTTCGGGCAAGGAT 254
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                                                                                                                                                                                                                                                      APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REPERENCE: PC009C1
CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2003
Prior Application removed - See File Wrapper or Palm
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 352
LENGTH: 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.2%; Score 293.8; DB 15;
96.1%; Pred. No. 3.5e-76;
"W.omatches 9;
                                                                                                                            CTTGAAGAGACATAT-GGACAATGAATCTGCAAA 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (59)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature
LOCATION: (482)
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; OTHER INFORMATION: n equals a,t,g, or
US-10-092-154-352
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                                                                                                                                                                                                                 Sequence 352, Application US/10092154 Publication No. US20030054375A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc_feature
LOCATION: (508)
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Matches 32
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RESULT 12 US-09-918-995-3654

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APPLICANT: Lo, Donald C.
APPLICANT: Donald C.
APPLICANT: Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Bath
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Ratz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING;
TITLE OF INVENTION: CELL DEATH
FILE OF INVENTION: CELL DEATH
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING;
TITLE OF INVENTION NUMBER: US/09/922,261
CURRENT FILING DATE: 2001-08-03
PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 414;
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Publication No. US2003007362341
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 230.6; DB 12;
Pred. No. 1.5e-57;
0; Mismatches 4;
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100.0%; Pred. No. 2.1e-53;
iive 0; Mismatches 0;
                                                                                                                                                                       CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEG ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3654
LENGTH: 414
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APPLICANT: COGENT NEUROSCIENCE,
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Best Local Similarity 98.3%;
Matches 233; Conservative
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Best Local Similarity 100.(
Matches 216; Conservative
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Job time : 403 secs
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CURRENT APPLICATION NUMBER: US/09/922,261

CURRENT FILING DATE: 1099-12-14
                                                     1489
                                                                                                                      1490 TCAGATAGCAGCTATGGTTCCCACTCCACTGACAGCCTCATGGGGTCCTCCCCTGTTTTC 1549
                                                                      121 TCAGATAGCAGCTATGGTTCCCACTCCACTGACGCCTCATGGGGTCCTCCCCTGTTTC 180
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1430 GTCTTCGAGGAGCCTATGTCAGGCATGAGTGAAGCTGGGATTCCTCAGAGCCCTGATGAC
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Pred. No. 1.2e-36;
0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                            Sequence 94, Application US/09922261
Patent No. US2002011471A1
GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 112, Application US/09922261 Patent No. US20020111471A1 GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.3%; Scor.
/ 100.0%; Pre
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Barney, Shawn
Thomas, Mary Beth
Portbury, Stuart D.
Puranam, Rasturi
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Barney, Shawn
Thomas, Mary Beth
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LENGTH: 159

TYPE: DNA

ORGANISM: Homo sapiens
US-09-922-261-94
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Best Local Similarity
Matches 159; Conserv
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US-09-922-261-112
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US-09-922-261-94
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APPLICANT:
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COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
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100.0%; Pred. No. 2.4e-31;
Mative 0; Mismatches 0;
       COMPOSITIONS AND METHODS
TITLE OF INVENTION: COMPOSITIONS AND METHODS:
TITLE OF INVENTION: AND TREATING CONDITIONS;
TITLE OF INVENTION: CELL DEATH
FILE REPERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/922, 261
CURRENT FILING DATE: 2001-08-03
PRIOR PELLOGATION NUMBER: US/09/461, 697
PRIOR FILING DATE: 1999-12-14
                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 112
LENGTH: 141
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                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-922-261-112
                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
tes 141; Conserv
                                                                                                                                                                                                                                                                                                       TYPE: DNA
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

July 18, 2003, 07:40:42; Search time 89 Seconds Run on:

(without alignments) 5895.775 Million cell updates/sec

Title: Perfect score: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

441362 segs, 153338381 residues Searched:

882724 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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/cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seg:\*
/cgn2\_6/ptodata/1/ina/pcTUS\_COMB.seg:\* Issued\_Patents\_NA:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Sequence 75, Appl	Sequence 76, Appl	80,	92,	96	100,	104,	94,	112,	114,	78, 4	88	116,	06	118,	84, 7	106,	120,	98,	1, 7		1, A	1,	Ĥ	Sequence 1, Appli	124	15, 7
SOFTERS	ID	US-09-461-697-75	US-09-461-697-76	US-09-461-697-80	US-09-461-697-92	US-09-461-697-96	US-09-461-697-100	US-09-461-697-104	US-09-461-697-94	US-09-461-697-112	US-09-461-697-114	US-09-461-697-78	US-09-461-697-88	US-09-461-697-116	US-09-461-697-90	US-09-461-697-118	US-09-461-697-84	US-09-461-697-106	US-09-461-697-120	US-09-461-697-98	US-09-234-332-1	US-09-461-697-108	US-08-552-142A-1	US-08-910-973-1	US-09-499-227-1	PCT-US95-05741-1	US-09-461-697-124	US-09-336-536-15
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оf	Query Match	75.3	72.1	63.8	35.1	29.8	19.6	12.6	9.3	8.2	7.7	6.1	5.6	5.3	5.1	4.2	4.0	3.5	3,3	3.0	2.8	2.8	2.2	2.5	2.5	2.5	2.3	2.2
	Score	1288	1233.2	1092	009	510	336	216	159	141	132	105	96	06	87	72	69	09	57	51	48.4	48	43.6	43.6	43.6	43.6	39	38.4
	Result No.	1	7	m	4	5	9	7	œ	đ	10	11	12	.13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

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Sequence 90, Appl Sequence 14, Appl Sequence 39, Appl Sequence 39, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 2, Appl Sequence 113, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 146, Appl Sequence 146, Appl Sequence 8, Appl Sequence 8	FOR DIAGNOSING DISORDERS, OR DISEASES INVOLVING	Length 1825;  i Indels 0; Gaps 0;  AAGCCAGACAGAGAGTTCC 403
4 US-09-149-476-90 1 US-08-232-465-14 4 US-09-078-294-6 4 US-09-284-393-39 4 US-09-285-171-39 4 US-08-569-749-3 5 PCT-US94-12912-3 5 PCT-US94-12912-3 5 PCT-US94-12912-2 4 US-09-149-476-316 4 US-09-149-476-316 4 US-08-085-122-12 4 US-08-085-122-12 4 US-08-943-71-146 4 US-08-232-191-8 4 US-09-232-191-8	. D METHODS FOR NDITIONS, DISC	Score 1288; DB 4; Pred. No. 0; 0 Mismatches 5 GGAGAGATACCATATCATC. GIGHIHITHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI
38 2.2 1821 5.4 2.1 18443 5.4 2.1 2525 5.4 2.1 2525 5.2 2.1 2601 5.2 2.1 2601 5.3 2.1 2601 5.3 2.1 2601 5.4 2.1 2601 5.5 2.1 2601 5.6 2.1 1571 6.6 2.1 2301 6.6 2.1 2301 6.6 2.1 2301 6.6 2.1 2301	SULT 1  *:09-461-697-75  *:09-461-697-75  Patent No. 6277974  GENERAL INFORMATION: APPLICANT: COGENT NEUROSCIENCE, Inc. APPLICANT: COGENT NEUROSCIENCE, Inc. APPLICANT: Barney, Shawn APPLICANT: Barney, Shawn APPLICANT: Portbury, Stuart D. APPLICANT: Portbury, Stuart D. APPLICANT: Portbury, Stuart D. APPLICANT: Portbury, Stuart D. APPLICANT: Fatz, Lawrence C. TITLE OF INVENTION: COMPOSITIONS AND M. TITLE OF INVENTION: COMPOSITIONS AND M. TITLE OF INVENTION: CELL DEATH FILE REFERENCE: 10001-005-999 CURRENT FILING DATE: 1999-12-14 NUMBER OF SEQ ID NOS: 466 SOFTWARE: FastSEQ for Windows Version SEQ ID NO 75 LENGTH: 1825 TYPE: DNA ORGANISM: HOMO Sapiens	1 8
C 298 31 36 2 4 4 4 3 3 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	RESULT 1 US-09-461-697-75 Sequence 75, Applic; Patent No. 6277974 GENERAL INFORMATION APPLICANT: COGENT APPLICANT: COGENT APPLICANT: Barney, APPLICANT: Barney, APPLICANT: Portburt; APPLICANT: Portburt; APPLICANT: Portburt; APPLICANT: Portburt; APPLICANT: Portburt; APPLICANT: Fatz, L. TITLE OF INVENTION; TITLE OF INVENTION; FILE REFERENCE: 10; CURRENT APPLICATION; CURRENT FILING DAT; LENGTH: 1825 LENGTH: DNA ORGANISM: HOMO Sal	Ouery Match Best Local Si Matches 1291.  Qy 344 i  Db 26 i  Oy 404 7  Oy 464 C

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> 76, Application US/09461697 . 6277974 US-09-461-697-76 Sequence 76 Patent No. RESULT

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TGGGTATTGGCAGTGTGCTCTCCCTCCAGAAGTTCTGGCAGCACCGCATCAAGGACTATC 1067

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APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo. Donald C.
APPLICANT: Lo. Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Barney, Shawn
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: PORTBURY: CAWFORCE C.
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CELL DEATH
FILE REPERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT PILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SSO ID NOS: 466
SSO ID NO 96
LENGTH: 510
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Pred. No. 5.9e-136;
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Patent No. 6277974
GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 29.8
Best Local Similarity 100.
Matches 510; Conservative
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US-09-461-697-96
   GENERAL INFORMATION:
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                                                                    APPLICANT: Barney, Shawn
APPLICANT: Barney, Shawn
APPLICANT: Barney, Shawn
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Fatz, Lawrence C.
APPLICANT: Fatz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-461-697-96
; Sequence 96, Application US/09461697
Sequence 92, Application US/09461697 Patent No. 6277974
                                                          APPLICANT: COGENT NEUROSCIENCE,
                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens US-09-461-697-92
                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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Best Local Similarity
Matches 216; Conserv
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APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Do. Donald C.
APPLICANT: Darney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Thomas, Mary Beth
APPLICANT: Portabury, Stuart D.
APPLICANT: Portabury, Stuart D.
APPLICANT: Watz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOUTHWARE: FastSEQ for Windows Version 4.0
                          APPLICANT: Katz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: COMPOSITIONS AND TITLE OF INVENTION: CLASSING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CELL DEATH
FILE REPERENCE: 10001-005-999
CURRENT APPLICATION UNMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1370 ATGGAGCCTCAAGAAAGTGAAGAAGGCAATGTCTCGGGCATGGTGTGCTGGGCAGTGAT 1429
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100.0%; Pred. No. 2.2e-86;
ive 0; Mismatches 0; Indels
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Patent No. 6277974
Portbury, Stuart D.
Puranam, Kasturi
                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 336; Conservative
                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-09-461-697-100
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LENGTH: 216
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DB 4; Length 216;

Score 216;

12.6%;

Query Match

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Sequence 94, Application US/09461697

Sequence 94, Application US/09461697

GENERAL INFORMATION:

APPLICANT: COGENT NEUROSCIENCE, Inc.

APPLICANT: Lo, Donald C.

APPLICANT: Barney, Shawn

APPLICANT: Puranam, Kasturi

APPLICANT: Puranam, Kasturi

APPLICANT: Puranam, Kasturi

APPLICANT: Puranam, Ratz, Lawrence C.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING

TITLE OF INVENTION: CALD-DEATH

TITLE OF INVENTION: CALL DEATH

STORMENT FILING DATE: 1999-12-14

NUMBER OF SEQ ID NOS: 466

SEQ ID NOS 466

SEQ ID NO 94
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                                                                                      1370 ATGGAGCCTCAAGAAAGTGAAGAAGGCAATGTCTCTGGGGCATGGTGTGCTGGGCAGTGAT
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Pred. No. 3e-52;
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100.0%; Pred. No. 4.8e-36;
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Best Local Similarity 100.0%; Pred. No. 4.86
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Patent No. 6277974
PARERAL INFORMATION:
APPLICANT: COGENT NBUROSCIENCE, Inc.
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APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
                                      Conservative
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APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Donald C.
APPLICANT: Donald C.
APPLICANT: Thomas, Mary Beth
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Ratz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CAMPOSITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CAMPOSITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CAMPOSITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CALL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo. Donald C.
APPLICANT: Lo. Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Ratz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CAUDENCETTIONS, DISORDERS, OR DISEASES INVOLVING;
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Pred. No. 3.5e-18;
iive 0; Mismatches 0;
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100.0%; Pred. No. 1e-20;
tive 0; Mismatches 0;
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                                                                                                                        ; Sequence 78, Application US/09461697
; Patent No. 6277974
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Best Local Similarity 100.0
Matches 96; Conservative
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Matches 105; Conservative
121 AGGAAAATATAA 132
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CORGANISM: Homo sapiens
US-09-461-697-78
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US-09-461-697-88
                                                                                                                                                                           GENERAL INFORMATION:
                                                                          RESULT 11
US-09-461-697-78
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SERBRAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Portbury, Stuart D.
APPLICANT: Puramas, Mary Beth
APPLICANT: Puramas, Kasturi
APPLICANT: Puramas, Kasturi
APPLICANT: Ratz, Lawrence C.
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CELL, DEATH
FILLE REFERENCE: 10001-005-999
CURRENT FILLING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 114
LENGTH: 132
                    APPLICANT: Katz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: COMPOSITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CELL DEATH
FILE REPERBURE: 10001-005-999
CURRENT APPLICATION UNDRES: US/09/461,697
CURRENT FILING DATE: 1999-12-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TCCACTGACAGCCTCATGGGGTCCTCCCTGTTTTCAACCAGCGCTGCAAGAAGAGGATG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
8.2%; Score 141; DB 4; I
Best Local Similarity 100.0%; Pred. No. 6.2e-31;
Matches 141; Conservative 0; Mismatches 0;
                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 112
LENGTH: 141
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APPLICANT: Puranam, Kasturi
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APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Puranence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CELL DEATH
FITLE OF INVENTION: CELL DEATH
FITLE OF PREPERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
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APPLICANT: Barney, Shawn
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Razz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
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SOFTHARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 116
LENGTH: 90
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 90
LENGTH: 87
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; BENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6277974
GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.
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Patent No. 6277974
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; ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-09-461-697-90
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US-09-461-697-116
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GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: Lo, Donald C.
APPLICANT: Homas, Mary Beth
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Raiz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 2.2e-11;
Matches 72; Conservative 0; Mismatches 0;
5.1%; Score 87; DB 4; I
100.0%; Pred. No. 1.2e-15;
Live 0; Mismatches 0;
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Patent No. 6277974
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87; Conservative
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US-09-461-697-118
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Human cell death

Human cell death p

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ААНВ4185 ААНВ4180 ААНВ4189 ААНВ4190 ААН14356 ААН14356

AAH84178 AAH84192 AAH84175 AAH84186 AAH84193 AAH84182 AAH84182

Lung cancer associ Murine neurogenic Mouse neurogenic d CDNA encoding muri

Human secreted pro Human secreted pro Human breast and o

ALIGNMENTS

Human prostate exp Human colon cancer Human cancer agent

AAS87900 ABV57087 AAH35032

AAV42928

442 1654 2089 2089 2572 168 1708 520

AAS60634 AAF97884 AAF97900

2355

DNA encoding novel

Human NeuroD1 gene Human cell death p Human polynucleoti

AAV24018 AAA62679 AAH84187

1340 1844 2502

AAF18137

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3. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1981.DAT;

4. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1981.DAT;

5. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1984.DAT;

5. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1988.DAT;

6. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1981.DAT;

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8. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1980.DAT;

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19. /SIDS2/gcgdata/geneseq/genesegn-embl/NA1990.DAT;

20. /SIDS2/gcgdata/geneseq/genesegn-embl/NA2000.DAT;

21. /SIDS2/gcgdata/geneseq/genesegn-embl/NA2001A.DAT;

22. /SIDS2/gcgdata/geneseq/genesegn-embl/NA2001B.DAT;

23. /SIDS2/gcgdata/geneseq/genesegn-embl/NA2001B.DAT;

24. /SIDS2/gcgdata/geneseq/genesegn-embl/NA2001B.DAT;

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Copyright (c) 1993 - 2003
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Human; tumour antigen protein; ART-1; HLA antigen; cytostatic; ds; bound cytotoxic T cell; tumour; cancer; remedy; prevent; diagnose. AAA62864 standard; DNA; 1711 BP Human ART-1 nucleotide sequence (SUMU ) SUMITOMO PHARM CO LTD (ITOH/) ITOH K. 99WO-JP06682 98JP-0341253 WPI; 2000-412318/35. P-PSDB; AAB03880. toh K, Gomi S; 40200032770-A1 Homo sapiens 30-NOV-1999; 01-DEC-1998; 08-JUN-2000 

Novel tumor antigen protein ART-1, tumor antigen peptide originating

Human protein enco Human secreted pro Human cell death p Human cell death p Human colNA for nov Human cell death p

AAA62864 AAH99786 AAC80572 AAH84170 AAH84171 AAC8418 AAC841981 AAC841981 AAC841981

22 22 22 23 25 25 25 25 25

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                                  CCACGCGGGCTTTGACTGTGCTAATGAGAGTGTCCTGGAGACCCTAACTGATGTGGCACA
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                                                      The invention relates to a novel human tumour antigen protein, ART-1. Included in the invention are polynucleotide sequences encoding the ART-1 proteins which when broken down intracellularly produce a tumour antigen peptide that can recognise HLA antigen and bound cytotoxic T cells. Antibodies which specifically recognise ART-1 and its derivative peptides, are also included in the invention. ART-1 exhibits cytostatic activity. The tumour antigen peptide originating from it, their derivatives, and DNAs are applicable in vivo or in vitro as remedies, preventives and
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applicable in vivo
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181 GTGACCGAGGAAACCCCTGGAGGGACTTGGGCATTCCTTGGGCTCCGTGCCTGTTCTTCG

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us-09-857-308-2.rng

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AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibatcerial; endocrine; cardiant; central nervous system; virucide; antibatcerial; endocrine; cardiant; central nervous system; virucide; antibatcerial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; antiagregant; haemostatic; vulnerary; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidiabetic; cytostatic; den therapy, antidepressant; nootropic; antidiabetic; cytostatic; neuroprotective antidiapetic; cytostatic; neuroprotein and polynucleotides are useful for screening for groduction, The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis; cof disorders associated with the activity of a protein e.g. inflammation, reuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, caneemia, platelet disorders, thrombocytopeenia, wounds, burns, ulcers, csteoporosis, severe combined immunodeficiency, eczema, allergic hintis, asthma, diabetes, cancer, multiple sclerosis, depression, and allergic and antidiatics.
                                                                                               Human; cancer; ulcer; HIV infection; human immunodeficiency virus;

antibiflammatory; antirheumatic; antiarthritic; immunosuppressive;

antibacterial; endocrine; cardiant; central nervous system; virucide;

antibacterial; endocrine; cardiovascular; antianaemic; anaemia;

antigagregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;

dermatological; antiallergic; antiathmatic; cytostatic;

neuroprotective; antidepressant; nootropic; antidiabetic; cytostatic;

munostimulant; gene therapy; antisense therapy; vaccine; inflammation;

immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;

cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;

qenetic disease; haematopoietic disorder; platelet disorder; asthma;

thrombocytopaenia; osteoporosis; severe combined immunodeficiency;

allergic rhinitis; diabetes; multiple solerosis; depression;

allergic rhinitis; disbetes; multiple solerosis; depression;

multiple solerosis; depression;

allergic rhinitis; disbetes; multiple solerosis; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polynucleotides encoding polypeptides, useful for liagnosis of e.g. cancer, ulcers and HIV infection
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                                                       Human protein encoding cDNA sequence SEQ ID NO:621
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21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
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P-PSDB; AAM25845.
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                                                                      416 CCACGGGAGTTCCGTCTGGTGGAAGTCCATGACCCACCCTGCACCCAACCCTCAGCCAAC
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Query Match 98.0 Best Local Similarity 99.6 Matches 1693; Conservative

DB 22; Length 6026;

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Nucleic acid molecules encoding
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ATGCTACAGATTAGTAAGCAACTCTCTGAAGAATATGAAAGGATTGTCAATCCTGAGAAG 4884
                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nonchropic; cerebroprotective; nonchropic; neuroprotective; antibacterial; virucide; funglicide; cancer; opthalmalogical; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; wound healing; nervous system disorder; aging; chemotaxis; ss.
                                              GAGGAGCCTATGTCAGGCATGAGTGAAGCTGGGATTCCTCAGAGCCCTGATGACTCAGAT
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99US-0172410.
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17-DEC-1999;
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Polynucleotide sequences AAC80531-C80580 represent cDNA encoding human secreted proteins AAB45120-B45169. Sequences AAB45170-B45255 represent alternative polypeptides encoded by the genes, and amino acid sequences to which they are homologous. The genes and proteins have activities to dependent on the tissues and cells in which they are expressed. Examples of their activities include immunosuppressive; antiarthritis; cardiant; vasotropic; vasotropic; cardiant; vasotropic; v
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encoding human secreted proteins, used in ameliorating a disorder, e.g. Alzheimer's deancers -
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99.0%;
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Homo sapiens

WO200145638-A2

28-JUN-2001

11-DEC-2000; 2000WO-US33547.

14-DEC-1999;

(COGE-) COGENT NEUROSCIENCE INC

Katz LC; ĸ, Puranam Portbury SD, Barney S, Thomas MB, Lo DC,

WPI; 2001-390297/41.

P-PSDB; AAG98644, AAG98645, AAG98646, AAG98647, AAG98648, AAG98649, AAG98650, AAG98651, AAG98652, AAG98653, AAG98657, AAG98656, AAG98659, AAG98659, AAG98659, AAG98660, AAG98661, AAG98665, AAG98666, AAG986665, AAG986666, AAG986669, AAG986669, AAG986669, AAG986670, AAG986671, AAG986672, AAG98670, AAG986671, AAG98672, AAG98673, 

ţ Novel protective sequence polynucleotides and polypeptides, used to identify modulators of their expression and activity, which are used to treat central nervous system conditions, diseases and disorders -

Example; Fig 1C; 325pp; English.

protect against call death (i.e., apoptosis or necrosis). Sequences which protect against call death (i.e., apoptosis or necrosis). Sequences which the part of the call death (i.e., apoptosis or necrosis). Sequences AARB4132, AARB4145, AARB4100, AARB4210, AARB4215, AARB4145. AARB4100, AARB4210, AARB4215, AARB4145. AARB4100 in the call death of the call of these cDNA clones. Sequences while the remaining nucleic acid sequences within the range given above represent the polypeptides encoded by the call death protective cDNA clones are able to prevent, delay or reverse progression through the apoptotic or necrotic pathways when injected into a call predisposed to or undergoing call death, protective nucleic acids and polypeptides can be used in the diagnosis and treatment of disorders associated with call death, and to screen for compounds which modulate their activity or expression. Such modulators, preferably a small organic molecule, an artibody, a ribozyme, or an antisense molecule, can also be used to treat the central nervous system including psychiatric or neurological disorders, especially ischemia-related conditions such as strokes, and also includes neurodegenerative disorders such as Alzheimer's disease, the modulators may also be used to treat infections such as include the retingence of the canting of diseases. The modulators may also be used to treat infections such as include the carbination of the canting to such as ischaemia related conditions such as such as cancers or benign tumours, blood collitors such as asthma or chronic obstructive pulmonary degeneration; hypertension; myocardial infarction; atherosclerosis; respiratory conditions such as asthma or chronic obstructive pulmonary degenerations because an anaemia; gastrointestinal conditions such as anaemia; gastrointestinal conditions such as anaemia; gastrointestinal conditions such as gastwa end and an anaemia agastrointestinal conditions such as gastwa end and an anaemia agastrointestinal conditions such as gastwa end and an anaemia agastr endometriosis; endocrine disorders such as Grave's disease or Hashimoto's thyroiditis; skin conditions such as dermatitis or urticaria; or immune Sequences AAH84132-AAH84370 represent human nucleic acid sequences which

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Cell death protective; apoptosis; necrosis; human; drug screening;

KW cell death-associated disorder; central nervous system disorder;

KW psychiatric disorder; neurological disorder; ischeamia-related disorder;

RICHART STRINGON; SIGNER STRINGON SIGNERS; Huntington's disease;

KW parkinson's disease; infection; meningitis; malaria; trypanosomiasis;

KW vascular disease; infection; meningitis; malaria; trypanosomiasis;

KW vascular disease; opthalmological disorder; diabetic retinopathy;

Macular degeneration; hypertension; myocardial infarction;

Atherosclerosis; respiratory disorder; asthma; transgenic animal;

Chronic obstructive pulmonary disease; neoplastic condition; cancer;

Chronic obstructive pulmonary disease; neoplastic condition; cancer;

Chronic obstructive pulmonary disease; biliary cirrhosis; kidney disorder;

Chromerulonephritis; liver disease; biliary cirrhosis; kidney disorder;

Chromerulonephritis; cystitis; endometriosis; endocrine disorder;

Chromerulonephritis; cystitis; endometriosis; endocrine disorder;

Chromerulonephritis; cystitis; endometriosis; endocrine disorder;

Chromerulonephritis; cystitis; endometriosis; kidney disorder;

Chromerulonephritis; cystitis; endometriosis; endocrine disorder;

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P-PSDB; AAG98644.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               system disorders such as acquired immunodeficiency syndrome (AIDS). nucled: caids may additionally be used to generate animal models of cell death-associated disorders. The present sequence represents a full-length cell death protective cDNA.
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                                                                                                                            DB 22; Length 1825;
                                                                                                                                                                   Indels
                                                                                        Sequence 1825 BP; 525 A; 447 C; 456 G; 397 T; 0 other;
                                                                                                                                                                   5;
                                                                                                           Score 1288; F
                                                                                                                                                                 0; Mismatches
                                                                                                                           75.3%;
ilarity 99.6%;
Conservative
                                                                                                                                                Similarity
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Matches 1291;
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Sequences AAH84132-AAH84370 represent human nucleic acid sequences which protect against cell death (i.e., apoptosis or necrosis). Sequences CC AAH84132, AAH84145, AAH84170, AAH84210, AAH84226, AAH84256, AAH84281, AAH84115, AAH84116, AAH84210, AAH84210, AAH84216, AAH84216, CC AAH84211, AAH84135 and AAH843167 represent 10 full-length CDNA clones, while the remaining nucleic acid sequences within the range given above represent the open reading frames (ORFS) of these CDNA clones. Sequences AAG98610-AAG98827 represent the Polypeptides convected by the cell death protective CDNA clones are able to protective ORFS. The cell death protective cDNA clones are able to prevent, delay or reverse progression through the apoptotic or necrotic companies and treatment of disorders and polypeptides can be companied to compounds which modulate their activity or certain the diagnosis and treatment of disorders associated with cell death, and to screen for compounds which modulate their activity or certain compounds which modulate their activity or certain for compounds which modulate their activity or antibody, a ribozyme, or an antisense molecule, can also be used to treat contral nervous system including psychiatric or neurological disorders such as strokes, and also includes Teurodegenerative disorders such as Alzheimer's disease, cused to treat infections such as meningitis, malaria, or trypanosomiasis; conference of treat infections such as disbetic retinopathy or macular celegeneration; hypertension; myocardial infarction; atherosolerosis; respiratory conditions such as centered or present or parking the contral contral conditions such as an entreal contral cont disease; neoplastic conditions such as cancers or benign tumours; blood cell conditions such as anaemia; gastrointestinal conditions such as pastrative colitis; liver conditions such as biliary cirrhosis; kidney disorders such as glomerulonephritis; cystitis; endometriosis; endocrine disorders such as Grave's disease or Hashimoto' thyroiditis; skin conditions such as dermatitis or unticaria; or immune system disorders such as acquired immunodeficiency syndrome (AIDS). nucleic acids may additionally be used to generate animal models of cell death-associated disorders. The present sequence represents a nervous system conditions, diseases and disorders Claim 2; Fig 6A; 325pp; English. cell death protective ORF. central ç 

Sequence 1239 BP; 309 A; 329 C; 318 G; 283 T; 0 other;

ö 407 467 121 527 181 587 241 647 301 707 361 767 61 348 TGCAAAGATACTGGGGAGAGATACCAATATCAAGCCAGACCAACAGAAGTTCCTTCG CAGCCAACAAGCCGACACTATGCTGGACATCCCCTCAGAGCCATGTAGTCTCA CCATCCATACGATTCAGTTGATTCAGCACAACCGACGTCTTCGCAACCTTATTGCCACAG CTCAGGCCCAGAATCAGCAGCAGACAGAAGGTGTAAAAAACTGAAGAGAGTGAACCCTCTTC CCTCGTGCCCTGGGTCACCTCCTCTCCTGATGACCTCCTGCCTTTAGATTGTAAGAATC CCAATGCACCATTCCAGATCCGGCACAGTGACCCAGAGAGTGACTTTTATCGTGGGAAAG DB 22; Length 1239; ·, 3; Indels Score 1233.2; Pred. No. 0; 0; Mismatches 72.18; 99.88; Conservative Similarity Best Local Sim Matches 1235; **#**08 62 528 588 648 Query Match Best Local S 168 122 708 ò g ð g ò g δ g ò g δ g

1127 1007 1067 1187 1247 1367 1427 1487 1307 1488 ACTCAGATAGCAGCTATGGTTCCCACTCCACTGACAGCCTCATGGGGTCCTCCCCTGTTT 1547 541 947 661 841 901 481 887 721 601 961 Human; ss; gene; secreted protein; immune deficiency; viral infection; bacterial infection; fungal infection; autoimmune disorder; burn; rheumatoid arthritis; multiple sclerosis; autoimmune thyroiditis; diabetes; allergy; asthm; neurodegenerative disease; Crohn's disease; Alzheimer's disease; Parkinson's disease; liver fibrosis; tumour; CCACAATCCTGGCCCACGCGGGCTTTGACTGTGCTAATGAGAGTGTCTCCTGGAGACCCTAA CCACAATCCTGGCCCACGCGGGCTTTGACTGTGCTAATGAGAGTGTCCTGGAGACCCTAA CTGATGTGGCACATGAGTATTGCCTTAAGTTTACCAAGTTGCTGCGGTTTTGCTGTGGACC CTGATGTGGCACATGAGTATTGCCTTAAGTTTACCAAGTTGCTGCGTTTTTGCTGTGGACC GGGAGGCCCGGCTGGGACAGACTCCTTTTCCTGATGTGATGGAGCAGGTATTCCATGAAG TGGGTATTGGCAGTGTGCTCTCCCTCCAGAAGTTCTGGCAGCACCGCATCAAGGACTATC ACAGTTACATGCTACAGATTAGTAAGCAACTCTCTGAAGAATATGAAAGGATTGTCAATC TCACTTTTCCTGTCAGTGAGGAGCTGGAGGCTGACCTTGCTTCTGGAGACCAGTCACTGC 1308 CACCACAGGCTTCAAGTGCAGAGGTAAATGCTTCTCCTCTTTGGAATCTGGCCCATGTGA 1368 AAATGGAGCCTCAAGAAAGTGAAGAAGGCAATGTCTCTGGGCATGGTGTGCTGGGCAGTG 1428 ATGTCTTCGAGGAGCCTATGTCAGGCATGAGTGAAGCTGGGATTCCTCAGAGCCCTGATG 1082 ATGTCTTCGAGGAGCCTATGTCAGGCATGAGTGAAGCTGGGATTCCTCAGAGCCCTGATG ACAGTTACATGCTACAGATTAGTAAGCAACTCTCTGAAGAATATGAAAGGATTGTCAATC CTGAGAAGGCCACAGAGGACGCTAAACCTGTGAAGATCAAGGAGGAACCTGTGAGGCGACA 1248 CTATGGGAGTGCTTGGGGCTCAGAGCGAACGCTTCCCATCTAACCTGGAGGTTGAAGCTT TCAACCAGCGCTGCAAGAAGAGGATGAGGAAAATATAA 1585 Human cDNA for novel secreted protein, SEQ ID 587. ВР ABK34818 standard; cDNA; 2606 (first entry) 1068 722 1128 1188 1548 482 888 542 948 1008 89/ 422 828 ABK34818; RESULT 6 ABK34818 q qq δ g g δ g ò g g δy g ŏ q ò qq οχ g ΟŊ q ŏ QΩ ò ò ò ò

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AAH84173
ID AAH84173 standard; cDNA; 1092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a variety of human tissue sources and which encode novel secreted proteins, their complements and sequences that hybridise to them. Also included are a vector comprising the polynucleotide, a host cell transformed with the vector, the proteins encoded by the cansformed with the vector, the proteins encoded by the polynucleotides, antibodies that bind to the proteins and identification of modulators of the proteins or the expression of the polynucleotide. The polynucleotides can be used as probes for the identification and isolation of full length cDNA and genomic DNA. The polynucleotides and isolation of full length cDNA and genomic DNA. The polynucleotides and isolation of full length cDNA and genomic DNA. The proteins are also be used as nutritional supplements. The protein is useful in the treatment of various immune deficiencies and disorders cutoimmune disorders (e.g. rheumatoid arthitis, multiple scalerosis, autoimmune thyroiditis and diabetes) and allergic reactions and cutoimmune thyroiditis and diabetes) and allergic reactions and usease, conditions (e.g. asthma). They are also useful for treating one togenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), liver fibrosis, coaquiation disorders (e.g. neemophilia), inflammatory disorders (e.g. crohd's disease) and tumours. They are also useful for resultating haematopolesis, for treating myeloid or lymphoid cell registration condition is one of the 625 CDNA sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to 625 polynucleotides which have been derived from
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                                                                                                                                                                                                                                                                                                                                                                                                             human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders
coagulation disorder; haemophilia; inflammatory disorder; ulcer;
tissue regeneration; wound healing; haematopoiesis; myeloid deficiency;
lymphoid cell deficiency.
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                                                                                                                                                                                                                                                                                                  Resnick
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                                                                                                                                                                                                                                                                                                  Agostino MJ,
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                              Clark HF, Fechtel
K, Graham JR;
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Best Local Similarity 99.7%;
Matches 1228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding a secreted protein.
                                                                                                                                                                                     29-MAR-2001; 2001WO-US10295
                                                                                                                                                                                                                        06-APR-2000; 2000US-194941P
                                                                                                                                                                                                                                                              (GEMY ) GENETICS INST INC
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                                                                                                           WO200177290-A2
                                                                          Homo sapiens
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W Cell death protective; apoptosis; necrosis; human; drug screening; W cell death-associated disorder; central nervous system disorder; W psychiatric disorder; neurological disorder; ischeamia related disorder; stroke disorder; stroke disorder; stroke disease; hifertion; ischeamic encephalopathy; neurodegenerative disease; hifertion; meningtits; malaria; trypanosomiasis; W parkinson's disease; hifertion; meningtits; malaria; trypanosomiasis; W parkinson's disease; pothalmological disorder; diabetic retinopathy; w ascular degeneration; hypertension; myocardial infarction; an ademia; paspliatory disorder; astham; transgenic animal; chronic obstructive pulmonary disease; neoplastic condition; cancer; W benign tumour; anaemia; gastrointestinal disorder; gastritis; willower disease; hillary cirrhosis; kidney disorder; glave's disease; Hashimoto's thyroiditis; skin condition; dermatitis; W urterata, immune disorder; acquired immunodeficiency syndrome; AIDS; Human cell death protective cDNA clone CNI-00714 ORF3, SEQ:80 Barney S, Thomas MB, Portbury SD, Claim 2; Fig 6C; 325pp; English. open reading frame; ORF; ss. 11-DEC-2000; 2000WO-US33547. 99US-0461697. (first entry) WPI; 2001-390297/41. P-PSDB; AAG98646. WO200145638-A2 Homo sapiens. 14-DEC-1999; 21-SEP-2001 DC, 2 

(COGE-) COGENT NEUROSCIENCE INC

Katz

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Puranam

Novel protective sequence polynucleotides and polypeptides, used to identify modulators of their expression and activity, which are used to treat central nervous system conditions, diseases and disorders -

in

Sequences AAH84132-AAH84370 represent human nucleic acid sequences which protect against cell death (i.e., apoptosis or necrosis). Sequences AAH84121, AAH84126, AAH84265, AAH844281, AAH84126, AAH84265, CC AAH84212, AAH84126, AAH84210, AAH84226, AAH84226, AAH844281, AAH84413, AAH84413, AAH84413, AAH84413, AAH84420, AAH84426, SC AAH844281, AAH844315 and AAH84367 represent 10 full-length cons. Sequences while the remaining nucleic acid sequences within the range given above consecutive ORFs. The cell death protective consecutive ORFs. The cell death protective consecutive ORFs. The cell death protective consecutive or necrotic pathways when injected into a cell predisposed to or undergoing cell cath. The cell death protective nucleic acids and polypeptides can be used in the diagnosis and treatment of disorders associated with cell death, and to screen for compounds which modulate their activity or expression. Such modulators, preferably a small organic molecule, an antisones molecule, can also be used to treat cell death-related diseases. Such diseases include those associated with the central nervous system including psychiatric or neurological disorders, especially ischaemia-related conditions such as Strokes, and also includes neurodegenerative disorders such as Alzheimer's disease, cused to treat infections such as meningitis, malaria, or trypanosomiasis; vascular diseases such as ischemic encephalopathy or cerebral conditions; eye conditions such as asthma or chronic obstructive pulmonary attact or expression; hypertension; myocardial infarction; atherosclerosis; cespinal paragraphy or macular diseases necessing each as asthma or chronic obstructive pulmonary attach as asthma or chronic or hadron the pulmonary attach as asthma or chronic or hadron the pulmonary attach as asthma or chronic or hadron the pulmonary attach as asthma or chronic or hadron the pulmonary attach as asthma or chronic or hadron the pulmonary attach. disease; neoplastic conditions such as cancers or benign tumours; blood

cirrhosis, kidney disorders such as glomerulonephritis; cystitis; endometriosis; endocrine disorders such as Grave's disease or Hashimoto' thyroiditis; skin conditions such as dermatitis or urticaria; or immune system disorders such as acquired immunodeficiency syndrome (AIDS). The nucleic acids may additionally be used to generate animal models of cell death-associated disorders. The present sequence represents a cell conditions such as anaemia; gastrointestinal conditions such as gastritis or ulcerative colitis; liver conditions such as biliary cell death protective ORF. 8888888888×8

Sequence 1092 BP; 269 A; 280 C; 287 G; 256 T; 0 other;

1033 1153 ö 1093 553 613 240 1154 CCTGTGAAGATCAAGGAGGAACCTGTGAGCGACATCACTTTTCCTGTCAGTGAGGAGCTG 1213 1334 AATGCTTCTCCTCTTTGGAATCTGGCCCATGTGAAAATGGAGCCTCAAGAAAGTGAAGAA 1393 120 673 180 733 793 540 GAGGCTGACCTTGCTTCTGGAGACCAGTCACTGCCTATGGGAGTGCTTGGGGCTCAGAGC 1273 300 853 360 913 420 973 480 099 009 720 780 9 CCTGATGACCTCCTGCCTTTAGATTGTAAGAATCCCAATGCACCATTCCAGATCCGGCAC 554 CACAACCGACGTCTTCGCAACCTTATTGCCACAGGCTCAGGCCCAGAATCAGCAGGAGACA 734 AGTGACCCAGAGAGTGACTTTTATCGTGGGAAAGGGGAACCTGTGACTGAACTCAGCTGG CACTCCTGTCGGCAGCTCCTCTACCAGGCAGTGGCCACAATCCTGGCCCACGCGGGCTTT AAGTTTACCAAGTTGCTGCGTTTTGCTGTGGACCGGGAGGCCCGGCTGGGACAGACTCCT GAAGGTGTAAAAACTGAAGAGAGTGAACCTCTTCCCTCGTGCCCTGGGTCACCTCCTCTC GACTGTGCTAATGAGAGTGTCCTGGAGACCCTAACTGATGTGGCACATGAGTATTGCCTT AAGTTTACCAAGTTGCTGCGTTTTGCTGTGGACCGGGAGGCCCGGCTGGGACAGACTCCT 481 TITCCTGATGTGATGGAGCAGGTATTCCATGAAGTGGGTATTGGCAGTGTGCTCCCTC CAGAAGTTCTGGCAGCACCGCATCAAGGACTATCACAGTTACATGACAGGTTAGTAAG 541 CAGAAGTTCTGGCAGCACCGCATCAAGGACTATCACAGTTACATGCTACAGATTAGTAAG 1094 CAACTCTCTGAAGAATATGAAAGGATTGTCAATCCTGAGAAGGCCACAGAGGACGCTAAA CAACTCTCTGAAGAATATGAAAGGATTGTCAATCCTGAGAAGGCCACAGAGGACGCTAAA GAACGCTTCCCATCTAACCTGGAGGTTGAAGCTTCACCACAGGCTTCAAGTGCAGAGGTA Gaps TTTCCTGATGTGATGGAGCAGGTATTCCATGAAGTGGGTATTGGCAGTGTGTCTCTCCTTC ö Length 1092; Indels ; DB 22; 5.3e-293; ö 63.8%; Score 1092; D 100.0%; Pred. No. 5.3 ive 0; Mismatches Best Local Similarity 100. Matches 1092; Conservative 421 674 914 Query Match 614 181 794 361 301 854 601 ò qq g Ω g à δ à δ qq ò g g δy g q δy a g δ ò ŏ ŏ δ g g οy q ò

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Sequence 1046 BP; 240 A; 304 C; 262 G; 240 T; 0 other;
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ATGAGTGAAGCTGGGATTCCTCAGAGCCCTGATGACTCAGATAGCAGCTATGGTTCCCAC
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        49.78;
96.18;
                               Conservative
        Query Match
Best Local Similarity
Matches 949; Conserv
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us-09-857-308-2.rng

RESULT 9

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protect against cell death (i.e., apoptosis or necrosis). Sequences which protect against cell death (i.e., apoptosis or necrosis). Sequences of AH84132-AH84105, AAH84201, AAH84205, AAH84205, AAH84201, AAH84201, AAH84205, AH84205, AH84201, AAH84201, AAH84301 caid sequences within the range given above represent the perfected within the range given above represent the polypeptides encoded by the cell death protective cDNA clones are able to protective ORFS. The cell death protective cDNA clones are able to protective ORFS. The cell death protective cDNA clones are able to prevent, delay or reverse progression through the apoptotic or necrotic pathways when injected into a cell predisposed to or undergoing cell death. The cell death protective nucleic soids and polypeptides can be used in the diagnosis and treatment of disorders associated with cell death. and to screen for compounds which modulate their activity or expression. Such modulators, preferably a small organic molecule, an antibody, a ribozyme, or an antisense molecule, can also be used to treat the central nervous system including psychiatric or neurological classofars, especially ischaemia-related conditions such as strokes, and also includes neurodegenerative disorders such as Alzheimer's disease, undergon's disease. The modulators may also be used to treat infections such as meningitis, malaria, or trypanosomiasis;
                                                                                                                                                                                                               cell death protective; apoptosis; necrosis; human; drug screening;

we cell death-associated disorder; central nervous system disorder;

psychlatric disorder; neurological disorder; ischaemia-related disorder;

we psychlatric disorder; neurological disorder; ischaemia-related disorder;

we proke; cerebral infarction; ischaemic encephalopath;

neurodegenerative disorder; Alzheimer's disease; Huntington's disease;

we parkinson's disease; infection; meningitis; malaria; trypanosomiasis;

we ascular disease; opthalmological disorder; diabetic retinopathy;

macular degeneration; hypertension; myocardial infarction;

whereosclerosis; respiratory disorder; diabetic retinopathy;

chronic obstructive pulmonary disease; neoplastic condition; cancer;

benign tumour; annemia; gastrointestinal disorder; gastritis;

ulcerative colitis; liver disease; biliary cirrhosis; kidney disorder;

drave's disease; Hashimoto's thyroditits; skin condition; dermatitis;

we reticaria; immune disorder; acquired immunodeficiency syndrome; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel protective sequence polynucleotides and polypeptides, used to identify modulators of their expression and activity, which are used in to treat central nervous system conditions, diseases and disorders -
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                                                                                                                                                                      Human cell death protective cDNA clone CNI-00714 ORF9, SEQ:92.
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                       AAH84179 standard; cDNA; 600 BP
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AAH84179
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          infarction; eye conditions such as diabetic retinopathy or macular degeneration; hypertension; myocardial infarction; atherosclerosis; respiratory conditions such as asthem or chronic obstructive pulmonary disease; neoplastic conditions such as cancers or benign tumours; blood cell conditions such as anaemia; gastrointestinal conditions such as gastritis or ulcerative collitis; liver conditions such as biliary cirrhosis; kidney disorders such as glomerulonephritis; cystitis; cystitis; thyroiditis; skin conditions such as dermatitis or urticaria; or immune system disorders such as dermatitis or urticaria; or immune system disorders such as acquired immunodeficiency syndrome (AIDS). The nucleic acids may additionally be used to generate animal models of cell death-associated disorders. The present sequence represents a cell death protective ORF.
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                                                                                                                                                                                                                                                                             Length 600;
                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                              Sequence 600 BP; 157 A; 138 C; 166 G; 139 T; 0 other;
                                                                                                                                                                                                                                                                             35.1%; Score 600; DB 22; I
100.0%; Pred. No. 2.3e-156;
ive 0; Mismatches 0;
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Cell death protective; apoptosis; necrosis; human; drug screening;

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cell death protective ORF.

Sox

endometriosis; endocrine disorders such as Grave's disease or Hashimoto's thyroiditis; skin conditions such as dermatitis or urticaria; or immune system disorders such as acquired immunodeficiency syndrome (AIDS). The nucleic acids may additionally be used to generate animal models of cell death-associated disorders. The present sequence represents a psychiatric disorder; neurological disorder; ischaemia-related disorder; stroke; cerebral infarction; ischaemic encephalopathy; neurodegenerative disorder: Alzhamer's disease; Huntington's disease; Parkinson's disease; Infection; meningitis; malaria; trypanosomiasis; vascular disease; othalmological disorder; diabetic retinopathy; macular degeneration; hypertension; myocardial infarction; atherosclerosis; respiratory disorder; asthma; transgenic animal; obstructive pulmonary disease; neoplastic condition; cancer; benign tumour; anaemia; gastrointestinal disorder; gastriits; ulcerative colitis; liver disease; biliary cirrhosis; kidney, disorder; grave's disease; Hashimoto's thyroiditis; skin condition; dermatitis; urticaria; immune disorder; sculricaria; immune disorder; acquired immunodeficiency syndrome; AIDS; Novel protective sequence polynucleotides and polypeptides, used to identify modulators of their expression and activity, which are used to treat central nervous system conditions, diseases and disorders -Lo DC, Barney S, Thomas MB, Portbury SD, Puranam K, Katz LC; cirrhosis; kidney disorders such as glomerulonephritis; cystitis death-associated disorder; central nervous system disorder; Claim 2; Fig 6K; 325pp; English. (COGE-) COGENT NEUROSCIENCE INC 11-DEC-2000; 2000WO-US33547 99US-0461697 open reading frame; ORF; ss WPI; 2001-390297/41. P-PSDB; AAG98654 WO200145638-A2. Homo sapiens 14-DEC-1999; 28-JUN-2001 

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                                                                                                                                            61 GCCACAGAGGACGCTAAACCTGTGAAGATCAAGGAGGAACCTGTGGGACGACATCACTTT
                                                                                                                                                                                                                                      1256 GTGCTTGGGGCTCAGAGCGAACGCTTCCCATCTAACCTGGAGGTTGAAGCTTCACCACAG
                                                                                                                                                                                                                                                   1316 GCTTCAAGTGCAGAGGTAAATGCTTCTCTCTTTGGAATCTGGCCCATGTGAAAATGGAG
                                                                                                                                                                                                                                                                                                                  241 GCTTCAAGTGCAGAGGTAAATGCTTCTCTTTTGGAATCTGGCCCATGTGAAAATGGAG
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                                                                             1076 AIGCTACAGATTAGTAAGCAACTCTCTGAAGAATATGAAAGGATTGTCAATCCTGAGAAG
                                                                                         1 ATGCTACAGATTAGTAAGCAACTCTCTGAAGAATATGAAAGGATTGTCAATCCTGAGAAG
                                                                                                                                                                                                                                                                                                                                                          136 GCCACAGAGGACGCTAAACCTGTGAAGATCAAGGAGGAACCTGTGAGCGACATCACTTTT
                                                                                                                                                                                  1196 CCTGTCAGTGAGGAGCTGGAGCTGACCTTGCTTCTGGAGACCAGTCACTGCCTATGGGA
                                                   Gaps
                                                   ;
                         Length 510;
                                                   Indels
Sequence 510 BP; 135 A; 116 C; 142 G; 117 T; 0 other;
                        29.8%; Score 510; DB 22; L 100.0%; Pred. No. 2.2e-131; ive 0; Mismatches 0;
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                         Query Match 29.89
Best Local Similarity 100.0
Matches 510; Conservative
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                                                                 The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORE has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dr primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences cDNA sequences have been obtained, the full 5' GTR is are longer 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
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                                                                                                                                                                                                                                                                                             1 ACGCGATCCTTGCCTCAGGCCTCTGGAGGTCCAGACAGCCGCCCAGCCCGCTCTGCGACG
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         nucleic acid that is a 5' expressed sequence tag (5' EST) for alming CDNAs and genomic DNAs that correspond to 5'ESTs and for
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                                                                                                                                                                                                                                           Length 544;
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                                                                                                                                                                                                                       Sequence 544 BP; 122 A; 164 C; 137 G; 120 T; 1 other;
                                                                                                                                                                                                                                         27.4%; Score 468; DB 21;
99.0%; Pred. No. 1.1e-119;
iive 0; Mismatches 0;
                                                Claim 1; SEQ ID 12485; 71pp + CD-ROM; English
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AAGCCGAA 544
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appendicitis;
chronic colitis;
Human digestive system antigen genomic sequence SEQ ID NO: 3567
                             Human; digestive system antigen; gene therapy; cancer; ulcerative colitis; infection; Hirschsprung's disease; digestive system disorder; Meckel's diverticulum; ds.
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2000US-0229509.
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19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
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17-MAR-2000;
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30-AUG-2000;
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27-SEP-2000;
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01-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 AATCTGCAAAGATACTGGGGAGAGATACCAATATCATCAAGCCAGACCAACAGAAGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTCCCTCGTGCCCTGGGTCACCTCCTCTCCTGATGACCTCCTGCCTTTAGATTGTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATCCCAATGCACCATTCCAGATCCGGCACAGTGACCCAGAGAGTGACTTTTATCG 759
                                                                                                                                                                                                                                                      The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of digestive system, particularly cancer and cancer metastases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cell death protective cDNA clone CNI-00714 ORF13, SEQ:100
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Pred. No. 2.6e-102;
                                                                                                                                                                                                                           Disclosure; SEQ ID NO 3567; 986pp; English.
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                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 23.8%;
Best Local Similarity 98.8%;
Matches 411; Conservative
08-DEC-2000; 2000US-0251989
08-DEC-2000; 2000US-0251990
11-DEC-2000; 2000US-0254097
                                           05-JAN-2001; 2001US-0259678
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                                                                                                      Rosen CA,
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Sequence 336 BP; 84 A; 78 C; 96 G; 78 T; 0 other;

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Novel protective sequence polynucleotides and polypeptides, used to identify modulators of their expression and activity, which are used in to treat central nervous system conditions, diseases and disorders neurodegenerative disorder; Alzheimmer's disease; Huntington's disease; Parkinson's disease; Infection; meningitis; malaria; trypanosomiasis; vascular disease; opthalmological disorder; diabetic retinopathy; macular degeneration; hypertension; myocardial infarction; atherosclerosis; respiratory disorder; asthma; transgenic animal; chronic obstructive pulmonary disease; neoplastic condition; cancer; benign tumour; anaemia; gastrointestinal disorder; gastriits; ulcerative colitis; liver disease; biliary cirrhosis; kidney disorder; growe's disease; Hashimoto's thyroiditis; swin condition; dermatitis; urticaria; immune disorder; acquired immunodeficiency syndrome; ADDS; Portbury SD, Puranam K, Katz LC; cerebral infarction; ischaemic encephalopathy; (COGE-) COGENT NEUROSCIENCE INC. Barney S, Thomas MB, 11-DEC-2000; 2000WO-US33547. 99US-0461697. open reading frame; ORF; ss WPI; 2001-390297/41. P-PSDB; AAG98656. WO200145638-A2. Homo sapiens. 14-DEC-1999; 28-JUN-2001. 2 2 3 

Sequences AAH84132-AAH84370 represent human nucleic acid sequences which protect against cell death (i.e., apoptosis or necrosis). Sequences AAH84121, AAH84120, AAH84120, AAH84255, AAH84120, AAH84120, AAH84120, AAH84255, AAH841281, AAH84120, AAH84120, AAH84255, AAH841281, AAH841315 and AAH84130, AAH84315 and AAH84367 represent the follows of the construction of the remaining nucleic acid sequences within the range given above CC represent the pollopeptides encoded by the cell death protective on construction of protective ORFs. The cell death protective construction of prevent, delay or rewerse progression through the apoptotic or necrotic pathways when injected into a cell predisposed to or undergoing cell death. The cell death protective nucleic acids and polypeptides can be used in the diagnosis and treatment of disorders associated with cell death, and to screen for compounds which modulate their activity or expression. Such modulators, preferably a small organic molecule, and the central nervous system including psychiatric or neurological calsorders, especially ischaemia-related conditions such as strokes, and also includes neurodegenerative diseases include those associated with cell calsorders, especially ischaemia-related conditions such as strokes, and also includes neurodegenerative diseases. The modulators may also be used to treat infections such as meningitis, malaria, or trypanosomiasis, recovered to treat infections such as meningitis, malaria, or trypanosomiasis, recovered to treat infections such as meningic and an analyzane or recovered to the second as meningic and the protections and also be also the contral calcolations such as meningic and also the calcolations and second as meningic and also the calcolations and also also the calcolations and also a vascular diseases such as inchemic encephalopathy or cerebral infarction; eye conditions such as diabetic retinopathy or macular diseases such as sichemic encephalopathy or macular infarction; eye conditions such as asthma or chronic obstructive pulmonary disease; neoplastic conditions such as cancers or benign tumours; blood cell conditions such as cancers or benign tumours; blood gastritis or ulcerative colitis; liver conditions such as placent conditions such as anaemia; gastrointestinal conditions such as cirrhosis; kidney disorders such as glomerulonephritis; cystitis; endometriosis; endocrine disorders such as grave's disease or Hashimoto's thyroiditis; skin conditions such as dermatitis or urticaria; or immune system disorders such as acquired immunodeficiency syndrome (AIDS). The nucleic acids may additionally be used to generate animal models of cell death-associated disorders. The present sequence represents a cell death protective ORF. Claim 2; Fig 6M; 325pp; English.

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                                                      1250 ATGGGAGTGCTTGGGGCTCAGAGCGAACGCTTCCCATCTAACCTGGAGGTTGAAGCTTCA 1309
                                                                                                      1310 CCACAGGCTTCAAGTGCAGAGGTAAATGCTTCTCCTCTTTGGAATCTGGCCCATGTGAAA 1369
                                                                                                                                                       1370 ATGGAGCCTCAAGAAAGTGAAGGCAATGTCTCTGGGCATGGTGTGCTGGGCAGTGAT 1429
                                                                                                                                                                                                                                                         1490 TCAGATAGCAGCTATGGTTCCCACTCCACTGACAGCCTCATGGGGTCCTCCCCTGTTTTC 1549
                                                                                                                                                                                                        1430 GTCTTCGAGGAGCCTATGTCAGGCATGAGTGAAGCTGGGATTCCTCAGAGCCCCTGATGAC 1489
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                                                                                                                    61 CCACAGGCTTCAAGTGCAGAGGTAAAATGCTTCTCCTCTTTGGAATCTGGCCCATGTGAAA 120
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                                                                             1 ATGGGAGTGCTTGGGGCTCAGAGCGAACGCTTCCCATCTAACCTGGAGGTTGAAGCTTCA
                                                                                                                                                                      cDNA encoding novel human connective tissue related polypeptide #342.
                              Gaps
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                             ;
     Length 336;
                              Indels
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                                                                                                                                                                                                                                                                                                                       301 AACCAGCGCTGCAAGAAGAGGATGAGGAAAATATAA 336
   Score 336; DB 22;
Pred. No. 4.2e-83;
                             Mismatches
   19.6%; Scc
ilarity 100.0%; Pr
Conservative 0;
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Query Match
Best Local Similarity
Matches 336; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; connective cytostatic; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200155343-A1.
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8-APR-2000;
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06-SEP-2000;
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26-SEP-2000;
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22-AUG-2000;
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08-SEP-2000;
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20-OCT-2000;
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                                              18-AUG-2000
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2000US-0246532 2000US-0246609 -NOV-2000; -NOV-2000; 17-NOV-2000; L7-NOV-2000; L7-NOV-2000; DEC-2000; 

(HUMA-) HUMAN GENOME SCI INC

Ruben SM; Rosen CA, Barash SC,

WPI; 2001-565190/63. P-PSDB; AAU86776.

Nucleic acid encoding novel connective tissue associated polypeptides, used in diagnosing, preventing, treating or ameliorating a disorder such as cancer or rheumatoid arthritis -

Claim 4; SEQ ID No 352; 673pp; English.

The present invention relates to the isolation of novel human connective tissue related polypeptides (AAU86435-AAU86923) and the polynucleotide (cDNA and genomic) sequences encoding them. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with connective tissue(s), including cancer. The polynucleotide sequences of the invention are also useful in gene therapy. ABK41613-ABK41611 represent cDNA sequences encoding the novel human connective tissue related polypeptides.

Once: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 517 BP; 108 A; 140 C; 132 G; 133 T; 4 other;

Gaps э; 17.2%; Score 293.8; DB 23; Length 517; 96.1%; Pred. No. 2.8e-71; ive 1; Mismatches 9; Indels 3; Conservative Query Match Best Local Similarity Matches 321; Conserv

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Claim 2; Fig 60; 325pp; English.

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cell death protective; apoptosis; necrosis; human; drug screening;
cell death-associated disorder; central nervous system disorder;
cell death-associated disorder; central nervous system disorder;
stroke; cerebral infarction; ischemic encephalopathy;
w psychiatric disorder; Alzheimer's disease; Huntington's disease;
w parkinson's disease; infection; meningitis; malaria; trypanosomisais;
w parkinson's disease; infection; meningitis; malaria; trypanosomisais;
w parkinson's disease; opthalmological disorder; diabetic retinopathy;
macular degeneration; hypertension; myocardial infarction;
w atherosclerosis; respiratory disorder; asthma; transgenic animal;
atherosclerosis; respiratory disorder; asthma; transgenic animal;
benign tumour; anaemia; gastrointestinal disorder; gastritis;
ulcerative colitis; liver disease; biliary cirrhosis; kidney disorder;
w glomerulonephritis; cystitis; endometriosis; endocrine disorder;
drave's disease; Hashimoto's thyrodititis; skin condition; dermatitis;
unique diseara; immune disporder; acquired immunodeficiency syndrome; AIDS;
                                                                    140
                                                                                    260
                                                                                                                                                     CCCACGCGTCCGAGACAGCCGCCCAGCCTCTGCGACGCANCAGTGAATAGTGTGGTA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel protective sequence polynucleotides and polypeptides, used to identify modulators of their expression and activity, which are used in to treat central nervous system conditions, diseases and disorders -
CTCTCGAGGTCCAGACAGCCGCCCAGCCCGCTCTGCGACGCAGCAGTAGTGTGGTA
                                                                                                                                     GACCTCAGGACCCTGTGATTGGCGCCTGCGCCGGACCGTGACCGAGGAAACCCCTGG
                                                                                                                                                                                                         AGGGACTTGGGCATTCCTTGGGCTCCGTGCCTGTTCTTCGTGCTCCTTTCGGGCAAGGAT
                                                                  CCTCCTTGTCTCGGTTCAGGTCCAGACCTCCCCGTCTTCCGGCTGCCCTGAACGTCAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cell death protective cDNA clone CNI-00714 ORF15, SEQ:104.
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                                                                                                                                                                                                                                                                                                                                                                CTTGAAGAGACATAT-GGACAATGAATCTGCAAA 353
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Sequences AAH84132-AAH84370 represent human nucleic acid sequences which protect against cell death (i.e., apoptosis or necrosis). Sequences CC protect against cell death (i.e., apoptosis or necrosis). Sequences CC AAH84281, AAH84126, AAH84126, AAH84126, AAH84281, AAH84126, AAH84126, AAH84281, AAH84135, and AAH84130, AAH84281, AAH84135, AAH84135, and AAH84130, AAH84281, AAH84281, AAH841315 and AAH84367 represent 10 full-length cDNA clones. Sequences while the remaining nucleic acid sequences within the range given above represent the open reading frames (ORFs) of these cDNA clones. Sequences AAG9810-AAG98109 represent the polypeptides encoded by the cell death protective only contective on reverse progression through the apoptotic or necrotic pathways when injected into a cell predisposed to or undergoing cell death. The cell death protective nucleic acids and polypeptides can be used in the diagnosis and treatment of disorders associated with cell death. The cell death protective nucleic acids and polypeptides can be used in the diagnosis and treatment of disorders associated with cell campinody, a ribozyme, or an antisense molecule, can also be used to treat central nervous system including psychiatric or neurological disorders, especially ischaemia-related conditions such as strokes, and also anticludes neurodegenerative disorders such as Alzheimer's disease, cused to treat infections such as meningitis, malaria, or trypanosomiasis; vascular diseases such as ischaemic encephalopathy or cerebral conditions such as asthma or chronic obstructive pulmonary degeneration; hypertension; myocardial infarction; atherosclerosis; resplanters conditions such as asthma or chronic obstructive pulmonary degeneration; hypertension; myocardial infarction; atherosclerosis; cell conditions such as asthma or chronic obstructive pulmonary degenerations when as asthma or chronic obstructive pulmonary conditions with as a such as dispensed or cell conditions such as astences or benigh tumous; such as aneamia; liver conditions such
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Matches 216; Conservative
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SUMMARIES

/cgn2\_6/ptodata/2/pubpa/uSi0\_NEW\_PUB.pep:\* /cgn2\_6/ptodata/2/pubpa/USi0\_PUBCOMB.pep:\* /cgn2\_6/ptodata/2/pubpa/USi0\_NEW\_PUB.pep:\* /cgn2\_6/ptodata/2/pubpaa/USi0\_PUBCOMB.pep:\*

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## ALIGNMENTS

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APPLICANT: POLIDLY, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Ratz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/922,261
PRIOR PAPLICATION NUMBER: US/09/461,697
PRIOR PAPLICATION NUMBER: US/09/461,697
PRIOR PELING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 77
                                                                                      Inc.
               Sequence 77, Application US/09922261
Patent No. US20020111471A1
GENERAL INFORMATION:
                                                                                  APPLICANT: COGENT NEUROSCIENCE,
APPLICANT: Lo. Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens US-09-922-261-77
US-09-922-261-77
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APPLICANT: Lo, Donald C.
APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Bath
APPLICANT: Thomas, Mary Beth
APPLICANT: Puranam, Rasturi
APPLICANT: Puranam, Rasturi
APPLICANT: Puranam, Rasturi
APPLICANT: Puranam, Rasturi
APPLICANT: Cawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: COMPOSITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US/09/461,697
PRIOR APPLICATION UNMER: US/09/461,697
PRIOR PLING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTHARE: FRASESQ for Windows Version 4.0
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APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Katz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
                      GNVSGHGVLGSDVFEEPMSGMSEAGIPOSPDDSDSSYGSHSTDSLMGSSPVFNQRCKKRM 411
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100.0%; Pred. No. 1e-
ive 0; Mismatches
                                                                                                                                                                                                 Sequence 93, Application US/09922261

Patent No. US20020111471A1

GENERAL INFORMATION:

APPLICANT: COGENT NEUROSCIENCE, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: COGENT NEUROSCIENCE, Inc.
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199; Conservative
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; ORGANISM: Homo sapiens
US-09-922-261-93
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RKI 363
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APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Thomas, Mary Beth
APPLICANT: Puranam, Kasturi
APPLICANT: CANTON: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CALL BATH
FILE OF INVENTION: CALL BATH
FILE OF INVENTION: CALL DATH
FILE OF INVENTION OF CALL BATH
FILE OF INVENTION NUMBER: US/09/922,261
CURRENT APPLICATION NUMBER: US/09/461,697
PRIOR PPLICANION NUMBER: US/09/461,697
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FASTSEQ for Windows Version 4.0
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 APFQIRHSDPESDFYRGKGEPVTELSWHSCRQLLYQAVATILAHAGFDCANESVLETLTD
                    183 VAHEYCLKFTKLLRFAVDREARLGQTPFPDVMEQVFHEVGIGSVLSLQKFWQHRIKDYHS
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100.0%; Pred. No. 6.5e-162;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 81, Application US/09922261 Patent No. US20020111471A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 87.3
Best Local Similarity 100.
Matches 363; Conservative
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US-09-922-261-105
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APPLICANT:
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APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: LO, Donald C.
APPLICANT: LO, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: PURANION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CELL DEATH
TITLE OF INVENTION: CELL DEATH
TITLE OF INVENTION: CELL DEATH
TITLE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/922,261
FRIOR FILING DATE: 2001-08-03
PRIOR PILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 101
LENGTH: 111
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                                                                                                                                                                                                                                                                                                  39.4%; Score 858; DB 11; Length 169; llarity 100.0%; Pred. No. 4.1e-69; Conservative 0; Mismatches 0; Indels
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TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/922,261
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US/09/461,697
PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 97
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Patent No. US20020111471A1
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Best Local Similarity 100.
Matches 111; Conservative
                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
US-09-922-261-97
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Best Local Si
Matches 169
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APPLICANT: POTEDLY, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Lawrence
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: ADD TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: ADD THEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: 02/09/461,697
PRIOR PILING DATE: 2001-08-03
PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/922,261
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US/09/461,697
PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 17.1%; Score 371; DB 11; Best Local Similarity 100.0%; Pred. No. 5.5e-26; Matches 71; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 2e-14;
tive 0; Mismatches
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APPLICANT: Lo. Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Katz, Lawrence C.
Sequence 105, Application US/09922261
Patent No. US20020111471A1
                                      GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, INC.
APPLICANT: Lo, Donald C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 113, Application US/09922261
Patent No. US20020111471A1
                                                                                                                                 Barney, Shawn
Thomas, Mary Beth
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Best Local Similarity 100.u
....hos 46; Conservative
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US-09-922-261-105
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RESULT

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FILING DATE: 03-APR-1996
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APPLICANT: Puranam, Kasturi D.
APPLICANT: Puranam, Kasturi D.
APPLICANT: Puranam, Kasturi D.
APPLICANT: Puranam, Kasturi D.
APPLICANT: Ratz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CELL DEATH
FILE OF INVENTION: CELL DEATH
FILE REPERBNCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
PRIOR FILING DATE: 1999-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCCONNELL, Stephen J.
INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
1 MSGMSEAGIPQSPDDSDSSYGSHSTDSLMGSSPVFNQRCKKRMRKI 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          372 MSEAGIPQSPDDSDSSYGSHSTDSLMGSSPVFNQRCKKRMRKI 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 10.3%; Score 224; DB 11; 1
Best Local Similarity 100.0%; Pred. No. 4e-13; Matches 43; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SPARKS, Andrew B.
HOFFMAN, NO. US20020034755A1h
RAY, Brian K.
FOWLKES, Dana M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/630,915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-JUn-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                    Sequence 115, Application US/09922261 Patent No. US20020111471A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USING SAME
                                                                                                                                                                               APPLICANT: COGENT NEUROSCIENCE, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 36, Application US/09879957 Patent No. US20020034755A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                    Barney, Shawn
Thomas, Mary Beth
Portbury, Stuart D.
Puranam, Kasturi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                     Lo, Donald C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
US-09-922-261-115
                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF
                                                                                             us-09-922-261-115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 115
                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 PVTELSWHSCRQLLYQAVATILAHAGFDCANESVLETLTDV----AHEYCLKFTKLLRF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 AISREANSKADPSLNPEQLKKLQDKIEKCKQDVLKTKEKYEKSLKELDQGTPQYMENMEQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219 VFHEVGIGSVLSLQKFWQHRIKDYHSYMLQISKQLS------EFYERIVNPEKAT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----ASGDOSLPMG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306 VLGAQSERFPSNLEVEASPQASSAEVNASPLWNLAHVKMEPQESEEGNVSGHGVLGSDVF 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 -----SKPSSTLNVPSNP-AQSAQSQSS------YNPFEDEDDT------GSTVS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 PIVREAFH--KQMMGGFKETKEAEDGFRKAQKPWAKKLKEVEAAKKAHHAACKEEKL--- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.4%; Score 118; DB 10; Length 377;
21.0%; Pred. No. 0.034;
Live 39; Mismatches 108; Indels 124; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------LGQTPFPDVMEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                366 EEP-----MSGMSEAGIPQSPDDSDSSYGSHSTDSLMGSSP 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267 EKDDTKAKNVSSYEKTOSYPTDWSDDESNNPFSSTDANGDSNP 309
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: WHYTE, DAVID
APPLICANT: WHYTE, DAVID
APPLICANT: CARNEPEEL, SEAN
APPLICANT: CHARYDEZK, GLEN
APPLICANT: CHARYDEZK, GLEN
APPLICANT: CHARYDEXK, GLEN
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT FILING DATE: 2001-06-26
PRIOR FILING DATE: 2000-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 EDAKPVKIKEEPVSDITFPVSEELEADL----
                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide SEQ ID NO: 36: US-09-879-957-36
                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 AVDREAR-----
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                                                                                                                                                                                                                                                                              LENGTH: 377 amino acids
                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 21.0%,
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
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SOFTWARE: Patentin Ver. 2
SEQ ID NO 67
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; ORGANISM: Homo sapiens
US-09-888-615-67
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314 RREKKKATDGFTLTGINQTGDQFLP-----SKPSSTLNVPSNP-AQSAQSQSS---- 360
                                                                                                                                                                                         ----ASGDQSLPMGVLGAQSERFPSNLEVEASPQASSAEVNASPLWN 338
                                                                                                                                                                                                                                                                                               -----YNPFEDEDDT------GSTVSEKEDIKAKNVSSYEKTQSYPTDWSDDESNNPFS 408
                                            192 KFTKLLRFAVDREARLGGTPFPDVMEQVFHEVGIGSVLSLQKFWQHRIKDYHSYMLQISK 251
                                                                              207 KYEKSL----KELDQGTPQYMENMEQVFEQ-----CQQFEEKRLRFFREVLLEVQK 253
                                                                                                                                                                                                                                                                LAHVKMEPQESEEGNVSGHGVLGSDVFEEP-----MSGMSEAGIPQSPDDSDSSYGSH 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 KFTKLLRFAVDREARLGQTPFPDVMEQVFHEVGIGSVLSLQKFWQHRIKDYHSYMLQISK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----ASGDQSLPMGVLGAQSERFPSNLEVEASPQASSAEVNASPLWN 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   339 LAHVKMEPQESEEGNVSGHGVLGSDVFEEP-----MSGMSEAGIPQSPDDSDSSYGSH 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Clapper, Jonathan D.
APPLICANT: Stolk, John A.
APPLICANT: Meagher, Madeleine J.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 KYEKSL----KELDQGTPQYMENMEQVFEQ-----CQQFEEKRLRFFREVLLEVQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |: : | || || || 254 HLNLSNVAGYKAIYHDLEQSIRAADAVEDLRWFRANHGPGMAMNWPQFEEWSADLIRTLS
                                                                                                                   252 QLS-----EEYERIVNPEKATEDAKPVKIKEEPVSDITFPVSEELEADL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 QLS-----EEYERIVNPEKATEDAKPVKIKEEPVSDITFPVSEELEADL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314 RREKKKATDGFTLTGINQTGDQFLP-----SKPSSTLNVPSNP-AQSAQSQSS---
       78; Gaps
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       Indels
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       83;
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0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.1%; Score 112; DB Best Local Similarity 22.4%; Pred. No. 0.17 Matches 56; Conservative 33; Mismatches
         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/833,263
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FASTSEQ FOR Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-10-025-380-685
; Sequence 685, Application US/10025380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 685, Application US/09833263
Patent No. US20020110547A1
GENERAL INFORMATION:
       33;
     Conservative
                                                                                                                                                                                                                                                                                                                                                                  STDANGDSNP 418
                                                                                                                                                                                                                                                                                                                                       STDSLMGSSP 401
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STDANGDSNP 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapien
US-09-833-263-685
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-09-833-263-685
       26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 685
LENGTH: 486
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                                                                                                                                                                                                                                                                                                     361
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       Matches
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                                          25;
                                                                                                                                                                            ----FKSSRTEPHCIIINLSTWIIWCYECDEKLSTHCNKKVLAQIVDFLQKHASKTQTS 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 IATAQAQNQQQTEGVKTEESEPLPSCPGSPPLPDDL-LPLDC-----KNPNAPFQIRHS 132
                                                                                                                                                                                                                                                                                                   ---LETLTDVAHE 188
                                                                                                                                                                                                                                                                                                                                   161 AFSRIMKLCEEKCETDEIQKGGKCRNLSVRGITNLGNTCFFNAVMQNLAQTYTLTDLMNE 220
                                                                                                                                                                                                                                                                                                                                                                          189 YCLKFTKLLRF-----AVDREARLGOTPFPDVMEQVFH---EVGIGSVLSLQKFWQ 236
                                                                                                                                                                                                                                                                                                                                                                                                            221 IKESSTKLKIFPSSDSQLDPLVVELSRPG--PLTSALFLFLHSMKETEKGPLSPKVLFNO 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----HRIKDYHSYMLQISKQL-----SEEYERIV-----NPEKATED---AK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LCQKAPRFKDFQQ---QDSQELLHYLLDAVRTEETKRIQASILKAFNNPTTKTADDETRK 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      272 PVKIK--EEPVSDITFPVSEE-LEADLASGDQSLPMGVLGAQSERFPSNLEVE--ASPQA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSAEVNASPLWNLAHVK------MEPQESEEGNVSGHGVLGSDVFEEPMSGMSEA 375
                                                                          32 VEVHDPPLHQP-SANKPKPPTMLDIPSE-----PCSLTIHTIQLIQHNRRLRNL 79
                                                                                                   Gaps
                                            168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
       DB 10; Length 783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 112; DB 10; Length 486; Pred. No. 0.17;
                                          Indels
                     ; Pred. No. 0.19;
61; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       376 GIPQSPDDSDSSYGSHSTDSL-MGSSPVFNQRCKKR 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            450 RLNESPTDDSEKEASHSESNVDADSEPSESSASKQ 485
5.3%; Score 115; 21.1%; Pred. No. 0
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CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FASLEEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 685, Application US/09922217
Patent No. US20020076414A1
GENERAL INFORMATION:
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Stolk, John A.
Wang, Tongtong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jiang, Yuqiu
Smith, Carole Lynn
King, Gordon E.
Wang, Aijun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.18; 22.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lodes, Michael J.
Secrist, Heather
Benson, Darin R.
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Xu, Jiangchun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CORGANISM: Homo sapiens
US-09-922-217-685
                     al Similarity
109; Conserv
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Best Local Similarity
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
     Query Match
                                                                                                                                                                                                                                                             106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   968
                       Best Local
Matches 10
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APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Sec
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SEQ ID NO 348
LENGTH: 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDSSYGSHSTDSLM-GSSPVFNQ 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       751 AEPVKESESSKSOVDGAGDVSNE 773
                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 2, Application US/10156634A; Publication No. US20030013152A1
                                                                                                                                                                                                                                                                                             Best Local Similarity 18.8 Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---ASGDQSLPMGVLGAQSERFPSNLEVEASPQASSAEVNASPLWN 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAHVKMEPQESEEGNVSGHGVLGSDVFEEP-----MSGMSEAGIPQSPDDSDSSYGSH 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 ----YNPFEDEDDT-----GSTVSEKEDIKAKNVSSYEKTQSYPTDWSDDESNNPFS 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 QLS-----EEYERIVNPEKATEDAKPVKIKEEPVSDITFPVSEELEADL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78;
                                                                                                                                                                                                                                                                        APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C14
CURRENT APPLICATION NUMBER: US/10/025,380
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 1129
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.1%; Score 112; DB
22.4%; Pred. No. 0.17
tive 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maxon, Mary
Milne, Todd
No. US20020128250Alman, Thea
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                                                                                                    Meagher, Madeleine Joy
Stolk, John A.
Wang, Tongtong
                                                                                                                                                                                                                Clapper, Jonathan D. Skeiky, Yasir A. W.
         US20020182191A1
                                                                                                                                                                                                                                               Fanger, Gary R.
Vedvick Thomas S.
                                                     Lodes, Michael J.
Secrist, Heather
Benson, Darin R.
                                                                                                                                                     Jiang, Yuqiu
Smith, Carole L.
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Matches 56; Conservative
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Wang, Aijun
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Madden, Kevin
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Silva, Jeff
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APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
                                          APPLICANT: Xu, Jianqchun
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Secondary Metabolite Production in Fungi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSE-----PCSLT1HT1QL1QHNRRLRNL1ATAQAQNQQQTEGVKTEESEPLPSCPGS 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307 PTQGPTSQNGPLSYNLPQVGLL-------PPQQQQQVSPLYDGNSITPPVKPST 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354 DQETYLTANRHGVSDQQYDSMAKTMNS-FQTTTIRHPMPLIATTNATGSNTSGTSASIIR 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 -PVTELSWHSCRQLLYQAVA---TILAHAGFDCANESVLETLTDVAHEYCLKFTKLLRFA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 ----PEKATEDAKPVKIKEEPVSDITFPVSEELEADLASGDQSL----PM--GVLG--A 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        512 DIQSVLKQNNPSNDSSSSSSSSTGIKSISPRTYYQPINNYQNPNGPSNISAAQLTYSSMNL 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 572 NNKIIPNNSIPAVSTIAAGEKPLKKCTMPNSNQLEGHTITNLQTLSATMPMKQQLMGNIA 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310 QSERFPSNLEVEASPQASSAEVNASPLWNLAHVKMEPQESEEGNV--------354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             355 ------SGHGVLGSDVFEEPMSGM-----SEAGIPQSPDD 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 GEIPISSSQTNRSSFDL--LPREFRLVEVHDPPLHQ------PSANKPKPPTMLDI 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 VDREARLGQTPFPDVMEQVFHEVGIGSVLSLQKFW------QHRIKDY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67; Mismatches 189; Indels 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 --HSYMLQIS-------KQLSEE--YERIVN-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 PP------LPDDLLPLDCKNPNAPFQ---IRHSDPESDFYRGKGE--
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TITLE OF INVENTION: Transcription Factors Related to TFIIA
FILE REFERENCE: 119941-11092
CURRENT APPLICATION NUMBER: US/10/156,634A
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 09/326,529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 11;
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                                                                                                                                                                                                                                       176 ES------VLETLTDVAHEYCLKFTKLLRFAVDREARLGQTPFPDVMEQV 219
                                                                                                                                                                                                                                                                                                        220 FHEVGIGSVLSLQKFWQHRIKDYHSYMLQISKQLSEEYERIVNPEKATEDAKPVKIK--E 277
                                                                                                                                                                                                                                                                                                                                                                          278 EPVSDITFPVSEE----LEADLASGDQ----SLPMGVLGAQSERFPSNLEVEASPQASSA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           272 Q------HDESLSTSPHGALHQHVTDIQLHILKNRMYGCDSVKQPRNIE 316
                                                                                                                                                                                                                                                                                                                                                                                                                                          212 NATSDILVSPGNEHKIVPEALLCHQESSHYISLPGVVFSPQVSQTNSDVESVLSGSASMA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GSDVFEEPMSGM 372
                                                                                                                                                                                      Gaps
                                                                                                                                                                                     84;
                                                                                                                                               Query Match 4.9%; Score 106; DB 15; Length 478; Best Local Similarity 22.9%; Pred. No. 0.57; Matches 72; Conservative 42; Mismatches 116; Indels 86
                                                                                                                                                                                                               128 QIRHSDPESDFYRGK-GEPVTELSW-HSCRQLLYQAVATILAHAG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 330 EVNASPLWNLAHVKMEPQESEEGNVSGHGVL----
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 20
SOFWHARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373 SEAGIPQSPDDSDS 386
                                                                                 ; TYPE: PRT; ORGANISM: Homo sapiens
US-10-156-634A-2
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Search completed: July 18, 2003, 10:02:38 Job time : 62.8436 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: July 18, 2003, 09:55:28; search time 31.3934 Seconds

(without alignments)
388.015 Million cell updates/sec

Title: US-09-857-308-1
Perfect score: 175
Sequence: 1 MMLQRYWGEIPISSSQTNRS......SIMGSSPVFNQRCKKRMRKI 414

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
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4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
7: /cgn2\_6/ptodata/1/iaa/packfiles1.pep:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued\_Patents\_AA:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 77. Appl	81,	93,	97,	101,	105,	113,	115,	22, 1	22,	22,	Sequence 22, Appl	22,	22;	22,	36,	24,	24,	24,	24,	24,	24,	24,	2, 4	4	4	375
SUMMARIES		-09-461	-461-697	-09-461-697-9	-09-461-697	-461-	US-09-461-697-113	-461-	-989-28(	-426-279	US-08-401-013-22	US-08-426-570-22	US-08-425-876-22	US-08-426-243-22	US-08-401-632-22	US-08-630-915A-36	US-07-999-280A-24	-6/	US-08-401-013-24	US-08-426-570-24	-425-87	1		US-09-326-529-2	US-09-326-529-4	-969-63	US-09-605-785-379
. 60	4	4	4	4	4	4	4	4	7	П	7	m	m	7	4	4	П	П	П	က	m	4	4	4	4	~	4
Length	412	363	199	169	111	71	46	43	552	552	552	552	552	552	552	377	552	552	552	552	552	552	552	478	1182	501	929
% Query Match		87.3	47.0	39.4	26.3	17.1	11.0	10.3	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.4	5.5	5.2	•	•	•	5.2	5.2	4.9	4.9	4.8	4.6
Score	2155	1898	1022	828	572	371	239	224	123	123	123	123	123	123	123	118	114	114	114	114	114	114	114	106	106	105	66
Result No.		7	က	4	5	9	7	<b>ω</b>	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

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Sequence 379, App Sequence 378, App Sequence 378, App Sequence 378, App Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 2, Appli	FOR DIAGNOSING DISORDERS, OR DISEASES INVOLVING	Length 412; 5; Indels 0; Gaps 0; SANKPRPPTMLDIPSEPCSLTI 64
US-09-439-313-379 US-09-552-616A-379 US-09-605-785-378 US-09-439-313-378 US-09-352-616A-378 US-08-473-119-4 US-08-475-352-4 5183884-4 US-07-853-913-4 US-08-175-352-4 US-08-177-310A-15 US-08-177-310A-15 US-08-57-139-2 US-08-57-139-2 US-08-56-138E-1 US-08-969-630-2 US-08-69-630-2 US-08-69-630-2 US-08-65-138E-1 US-08-69-630-2 US-08-69-630-2 US-08-69-630-2 US-08-69-630-2 US-08-69-630-2 US-08-69-630-2 US-08-69-630-2 US-08-444-48-9 US-08-69-630-2 US-08-69-630-2	ALIGNMENTS  1697  Inc. S AND METHODS FOR G CONDITIONS, DISO 09/461,697  ersion 4.0	Score 2155; DB 4; Pred. No. 4.9e-20 0; Mismatches 0 DLLPREFLVEVHDPPLHQP LLPREFLVEVHDPPLHQP LLPREFLVEVHDPPLHQP LLPREFLVEVHDPPLHQP LLPREFLVEVHDPLHQP LLI
4.6 656 4.6 656 4.6 1719 4.6 1719 4.5 1719 4.5 1719 4.5 1719 4.5 1719 4.5 1719 4.5 1719 4.5 1719 4.5 1734 5.5 1734 5.5 1734 5.6 1734 5.6 1734 5.7 1	ation US,  E. Shawn Mary Bet Nary Bet Y, Kasturi Y, Kasturi OCELL DI OOI-005 N NUMBER E: 1999-7 OS: 466 For Winde	99.1%; 0; Conservative RVWGEIPISSSOTNRSSEI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
28 30 30 31 31 32 33 34 35 36 36 37 37 38 38 37 40 40 40 40 41 41 42 41 44 44 44 45 44 46 46 47 46 47 46 47 46 47 46 47 47 46 47 47 47 47 47 47 47 47 47 47 47 47 47	SULT 1 -09-461- Sactent C Sactent C APPLICA AP	Query Match Best Local S Matches 410  8 3  65 61 125 123 185
		6 6 6 6 6 6

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COGENT NEUROSCIENCE, Inc.
                    Lo, Donald C.
                                                                                                                                                                                                                                                       TYPE: PRT
CRGANISM: Homo sapiens
US-09-461-697-93
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US-09-461-697-97
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Sequence 81, Application US/09461697

Sequence 81, Application US/09461697

GENERAL INFORMATION:

APPLICANT: COGENT NEUROSCIENCE, Inc.

APPLICANT: Lo, Donald C.

APPLICANT: Thomas, Mary Beth

APPLICANT: Puranam, Kasturi

APPLICANT: Puranam, Kasturi

APPLICANT: Retz, Lawrence C.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING

TITLE OF INVENTION: CELL DEATH

FILE REFERENCE: 10001-005-999

CURRENT APPLICATION NUMBER: US/09/461,697

CURRENT FILING DATE: 1999-12-14

NUMBER OF SEQ ID NOS: 466

SOFTWARE: FastSEQ for Windows Version 4.0
                   52 MLDIPSEPCSLTIHTIQLIQHNRRLRNLIATAQAQNQQQTEGVKTEESEPLPSCPGSPPL 111
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305 GVLGAQSERFPSNLEVEASPQASSAEVNASPLWNLAHVKMEPQESEEGNVSGHGVLGSDV 364
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Mismatches
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Patent No. 6277974
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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US-09-461-697-81
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APPLICANT: Barney, Shawn
APPLICANT: Homas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Watz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 93
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100.0%; Pred. No. 3.5e-77;
ive 0; Mismatches 0;
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APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: Thomas, Mary Beth
APPLICANT: Thomas, Mary Beth
APPLICANT: Thomas, Mary Beth
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Rasturi
APPLICANT: AND TREATING CONDITIONS, DISC
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT FRILING DATE: 1999-12-14
CURRENT FRILING DATE: 1999-12-14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 466
FEWALD OF TREATMENT: 100
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Best Local Similarity 100.
Matches 169; Conservative
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ORGANISM: Homo sapiens
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Matches 46; Conserv
                          ; ORGANISM: HOMC
US-09-461-697-105
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Patent No. 6277974

GENERAL INFORMATION:

APPLICANT: COGENT WEUROSCIENCE, Inc.

APPLICANT: Lo, Donald C.

APPLICANT: Homas, Mary Beth

APPLICANT: Puranum, Kasturi

APPLICANT: Puranum, Kasturi

APPLICANT: Puranum, Kasturi

APPLICANT: Puranum, Kasturi

APPLICANT: Puranum, Rasturi

APPLICANT: Puranum, Rasturi

APPLICANT: Puranum, Rasturi

APPLICANT: Puranum, Rasturi

APPLICANT: Ratz, Lawrence C.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING

TITLE OF INVENTION: CELL DEATH

FILE REFERENCE: 10001-005-999

CURRENT APPLICATION NUMBER: US/09/461,697

CURRENT FILING DATE: 1999-12-14

NUMBER OF SEQ ID NOS: 466

SOUTHWARE FRASEEQ FOR Windows Version 4.0
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APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: BATNEY, Shawn
APPLICANT: Thomas; Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranem, Kasturi
APPLICANT: Puranem, Kasturi
APPLICANT: Puranem: Raturi
APPLICANT: Ratz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: COMPOSITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
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Gaps
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100.0%; Pred. No. 3.8e-49;
tive 0; Mismatches 0;
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Patent No. 6277974
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Best Local Similarity
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LENGTH: 71
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Puranam, Kasturi
APPLICANT: APPLICANTON: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FSSTEQ for Windows Version 4.0
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Sequence 115, Application US/09461697

Sequence 115, Application US/09461697

GENERAL INFORMATION:

APPLICANT: COGENT WERROSCIENCE, Inc.

APPLICANT: Lo, Donald C.

APPLICANT: Puranas, Mary Beth

APPLICANT: Puranas, Mary Beth

APPLICANT: Puranas, Mary Beth

APPLICANT: Raiz, Lawrence C.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING

TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING

TITLE OF INVENTION: CELL DEATH

FILE REFERENCE: 10001-005-999

CURRENT APPLICATION NUMBER: US/09/461,697

CURRENT FILING DATE: 1999-12-14

NUMBER OF SEQ ID NOS: 466

SOFTWARE: FastSEQ for Windows Version 4.0
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   Length 71;
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Query Match 17.1%; Score 371; DB 4; Best Local Similarity 100.0%; Pred. No. 1.5e-29; Matches 71; Conservative 0; Mismatches 0;
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US-09-461-697-113
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                                                                194 TKLLRFAVDREARLGQTPFP-----DVMEQVFHEVG----IGSVLSLQKFWQHRIK 240
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                                                                                                                                                                                                                                      301 SLPMGVL----GAQSERFPSNLEVEASPQASS---AEVNASPLWNLAHVKMEPQESEEGN 353
                                                                                                                                                                                                                                                               14 SSQTNRSSFDLLPREFRLVEVHDPPLHQPSANKPKPPTMLDIPSEPCSLTIHTIQLIQHN 73
                                                                                                                                                                                                                                                                                                                           ---- PQSPDDSDSSYGSHSTDSL 396
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                                                                                                      332 ---IQAETDRPRALSASPFPKSTEDQKPVDITDRPLTEVNPMRPIGOT--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.7%; Score 123; DB 1; 21.6%; Pred. No. 0.0016;
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                                                                                                                                                                                                                                                                                                                           354 VSGHGVLGSDVFEEPMSG-----MSEAGI----
      295 -ESSL--GTNWVLEEASGEASEGFLTQ-
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FILING DATE: 21-APR-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: McGarrigle Jr., Philip L.
REGISTRATION NUMBER: 31,395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/08426279 Patent No. 5672343
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NOBLE, JANELLE A.
MARTIN, GEORGE A.
KAWASAKI, ERNEST S.
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TELEPHONE: (510) 601-2718
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(510) 655-3542
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NEW NUMBER OF SEQUENCES: 2. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Emveryville
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --- 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 552;
                                                                                                        ch 10.3%; Score 224; DB 4; Length 43; Similarity 100.0%; Pred. No. 2.5e-15; 43; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                            372 MSEAGIPQSPDDSDSSYGSHSTDSLMGSSPVFNQRCKKRMRKI 414
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Intellectual Property - R440, P.O. Box 8097
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ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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FILING DATE: 28-DEC-1992
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NAME: MCGARTIGLE Jr., Philip L.
REGISTRATION NUMBER: 31,395.
REFERENCE/DOCKET NUMBER: 0681.007
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/07999280A Patent No. 5573930 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KAWASAKI, ERNEST S.
APPLICANT: COVNE, MAZIE YEE
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: KOTHS, KIRSTON E.
                                                                                                                                                                                                                                                                                                                                                                                                             LADNER, MARTHA B. NOBLE, JANELLE A. MARTIN, GEORGE A.
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Best Local Similarity 21.6%;
Matches 90; Conservative 4
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amino acid
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; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-461-697-115
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STATE: California
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Best Local Similarity
Matches 43; Conserv
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APPLICANT:
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JS-08-426-570-22
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RRLRNLIATAQAQNQQQTEGVKTEESEPLPSCPGSPPLPDDLLPLDCKNPNAPFQIRHSD 133
                                                                   134 PESDFYRGKGEPVTELSWHSCROLLYQAVATILAHAGFDCANESVLETLTDVAHEYCLKF 193
                                                                                                        ----- EAKFSPSTPVGGS---- 331
                                                                                                                                                                  241 DYHSYMLQISKQLSEEYERIVNPEKATEDAKPVKIKEEPVSDITFPVSEELEADLASGDQ 300
                                                                                                                                                                                                                                                                                301 SLPMGVL----GAQSERFPSNLEVEASPQASS----AEVNASPLWNLAHVKMEPQESEEGN 353
                                                                                                                                                                                                                                                                                                      -SSDPQIPESVFHLLVPGILLVLTVGGLLFYKWKWRSHRDPQTLDSSVGRPEDSSL 540
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                                  -----TEDSOPHPSAGGPVPGVEDIL
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STREET: Intellectual Property - R440, P.O. Box 8097
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                                                                                                    295 -ESSL--GINWVLEEASGEASEGFLTQ-----
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
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PROFILE APPLICATION NATA:
APPLICATION NUMBER: US 07/999,280
FILING DATE: 28-DEC-1992
ATTORNEY AGENT INFORMATION:
NAME: MCGATIGLE JT., Philip L.
REGISTATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0681.007
TELECOMMUNICATION INFORMATION:
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FILING DATE: 08-MAR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KAWASAKI, ERNEST S.
APPLICANT: COVINE, MAZIE YEE
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: KOTHS, KIRSTON B.
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amino acid
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INFORMATION FOR SEQ ID NO:
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                                271 DRL-----
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94662-8097
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194 TKLLRFAVDREARLGQTPFP-----DVMEQVFHEVG----IGSVLSLQKFWQHRIK 240
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                                                                                                                                                                                                                                  294
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                                                                                            14 SSQTNRSSFDLLPREFRLVEVHDPPLHQPSANKPKPPTMLDIPSEPCSLTIHTIQLIQHN
                                                                                                                                                                                   74 RRLRNLIATAQAQNQQQTEGVKTEESEPLPSCPGSPPLPDDLLPLDCKNPNAPFQIRHSD
                                                                                                                                                                                                                                                                                                                              -----EAKFSPSTPVGGS-----
                                                Gaps
                                                                                                                                                                                                                                  271 DRL------TEDSQPHPSAGGPVPGVEDIL-------
Score 123; DB 1; Length 552;
Pred. No. 0.0016;
7; Mismatches 144; Indels 136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: CHIRON CORPORATION STREET: Intellectual Property - R440, P.O. Box 8097 CITY: Emveryville STATE: California
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                                                                                                                                                                                                                                                                                                                            295 -ESSL--GINWVLEEASGEASEGFLTQ----
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NAME: MCGALTIGLE Jr., Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0681.012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC.COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: HALENBECK, ROBERT F.
APPLICANT: KOTHS, KIRSTON E.
TITLE OF INVENTION: NEW FORMS O
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                              47:
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NOBLE, JANELLE A.
MARTIN, GEORGE A.
KAWASAKI, ERNEST S
5.7%;
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(510) 655-3542
                                              Conservative
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FILING DATE: 21-APR
CLASSIFICATION: 530
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Query Match
Best Local Similarity
Matches 90; Conserv
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                                                                                                                                                                                                                             14 SSQTNRSSFDLLPREFRLVEVHDPPLHQPSANKPKPPTMLDIPSEPCSLTIHTIQLIQHN
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                                                                                                                                                                                          Mismatches 144; Indels 136;
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APPLICANT: COVNE, MAZIE YEE
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: KOTHS, KIRSTON E.
TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
                                                                                                                                                                                                                                                                                                                                          271 DRL-----TEDSQPHPSAGGPVPGVEDIL-----
                                                                                                                                                       Length 552;
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                                                                                                                                                     Score 123; DB 3;
Pred. No. 0.0016;
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Intellectual Property - R440, P.O.
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FILING DATE: 21-APR-1995
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: McGarrigle Jr., Philip L.
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APPLICANT: LADNER MARTHA B.
                                                                                                                                                                                        47;
                                                                                                                                                     5.78;
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 552 amino acids TYPE: amino acid
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                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-426-570-22
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               271 DRL------TEDSQPHPSAGGPVPGVEDIL------
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APPLICANT: LADNER, MARTHA B.
APPLICANT: NOBLE, JANELLE A.
APPLICANT: MARTIN, GEORGE A.
APPLICANT: KAWASAKI, ERREST S.
APPLICANT: COYNE, MAZIE YEE
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: KOTHS, KIRSTON E.
TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                             5.7%; Score 123; DB 3; Length 552; 21.6%; Pred. No. 0.0016;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     47; Mismatches 144;
                      0681.011
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31,395
                REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
                                                                                                     (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 21.6
Matches 90; Conservative
                                                                                                                                 TELEX: n/a
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
REGISTRATION NUMBER:
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STATE: California
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TELEFAX: (
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TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 DYHSYMLQISKQLSEEYERIVNPEKATEDAKPVKIKEEPVSDITFPVSEELEADLASGDQ 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -ESSL--GINWVLEEASGEASEGFLTQ------EAKFSPSTPVGGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 SSQTNRSSFDLLPREFRLVEVHDPPLHQPSANKPKPPTMLDIPSEPCSLTIHTIQLIQHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.7%; Score 123; DB 4; Length 552; Best Local Similarity 21.6%; Pred. No. 0.0016; Matches 90; Conservative 47; Mismatches 144; Indels 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KOTHS, KIRSTON E.
TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
UNDER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Intellectual Property - R440, P.O. Box 8097
                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/999,280
FILING DATE: 28-DEC-1992
ATTOCNEY AGENT INFORMATION:
NAME: MCGARTIGLE JT., Philip L.
REGISTRATION NUMBER: 31,395
REFERNCE/DOCKET NUMBER: 31,395
REERECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2718
                           APPLICATION NUMBER: US/08/426,243 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/08401632
Patent No. 6204020
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LADNER, MARTHA B.
NOBLE, JANELLE A.
MARTIN, GEORGE A.
COYNE, MAZIE YEE
HALENBECK, ROBERT F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHIRON CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: n/a
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-426-243-22
                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:

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226 SQRTEGSS--LLPSELPL-----RIEDPGSAKQRP-----PRSTCQ-TLESTEQPNHG 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 PESDFYRGKGEPVTELSWHSCRQLLYQAVATILAHAGFDCANESVLETLTDVAHEYCLKF 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332 ---IQAETDRPRALSASPFPKSTEDQKPVDITDRPLTEVNPMRPIGQT-----QNNTP 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 DYHSYMLQISKQLSEEYERIVNPEKATEDAKPVKIKEEPVSDITFPVSEELEADLASGDQ 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 VSGHGVLGSDVFEEPMSG-----MSEAGI------PQSPDDSDSSYGSHSTDSL 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -SSDPQIPESVFHLLVPGIILVLLTVGGLLFYKWKWRSHRDPQTLDSSVGRPEDSSL 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 TKLLRFAVDREARLGQTPFP-----DVMEQVFHEVG----IGSVLSLQKFWQHRIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271 DRL-----TEDSQPHPSAGGPVPGVEDIL-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295 -ESSL--GINWVLEEASGEASEGFLIQ------EAKFSPSIPVGGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.7%; Score 123; DB 4; Length 552;
ilarity 21.6%; Pred. No. 0.0016;
Conservative 47; Mismatches 144; Indels 136;
                                                 COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: EL POPPY disk
COMPUTER: TEM PC COMPATIBLE
CORRENT G SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,632
FILING DATE: 09-MAR-1995
CLASSIFICATION: 536
ATTONREY/AGENT INFORMATION:
NAME: MCGATTIGLE JT., Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/POCKET UMBER: 31,395
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (510) 601-2718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS: LEWITH: 552 amin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-401-632-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 90; Conserv
N: U.S.A.
94662-8097
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Search completed: July 18, 2003, 10:01:22 Job time : 34.3934 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 18, 2003, 09:03:57; Search time 25.5071 Seconds (without alignments) 673.193 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-857-308-1 2175 1 MNLQRYWGEIPISSSQTNRS......SLMGSSPVFNQRCKKRMRKI 414

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

. 112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P07141 mus musculu	homo	bacil	P35177 saccharomyc	P53438 saccharomyc	Q9wve8 mus musculu	Q12114 saccharomyc	Q92538 homo sapien	tarsi	homo	Q9y6q2 homo sapien	homod	rattu	homo	homo	homo	h vac	P30414 homo sapien	mus n	P87078 candida alb	_	P05770 papio anubi	borre			P29681 drosophila	Q61670 mus musculu		O60583 homo sapien		P23226 drosophila	5570 rattus	P50478 gallus gall
SUMMARIES	ID	CSF1_MOUSE	PAC2_HUMAN	SP6D_BACSU	SPT7_YEAST	SOK2_YEAST	PAC2_MOUSE	CHS5_YEAST	GBF1_HUMAN	INVO_TARBA	T2AY_HUMAN	T2AZ_HUMAN	ANK3_HUMAN	PAC2_RAT	Y249_HUMAN	SAL1_HUMAN	FA5_HUMAN	VPP3_HUMAN	NKCR_HUMAN	PGCV_MOUSE	TOP2_CANAL	PGCV_BOVIN	APE_PAPAN	VATB_BORBU	Y298_HUMAN	PVDB_PLAKN	IMP2_DROME	HLX1_MOUSE	DCPY_ZYMMO	CCT2_HUMAN	NEB1_RAT	MAPX_DROME	IRS1_RAT	AMPH_CHICK
	DB	-	М	7	7	Н	<del></del> 1	Н	Н	-	Н	-	Н	Н	-	7	-	-1	-	-	Н			Н	-	-	1	7	~	↔	-	Н	П	П
	Query Match Length	552	486	575	1332	785	486		1859				4				2224		1462	3358	1461	3381	317	434	901	1153	466	476	268	730	1095	1185	1235	682
æ	Query Match	5.7	5.4	5.4	5.2	5.1		5.0	4.9	4	4.9	4.9	4.9	4.8	4.8	4.8	4.8	4.7	4.7	4.7	4.7	4.7	4.6	4	4	4	4	4	4.6	4	4	4	4.6	4.5
	Score	123	117	117	112.5	110.5	109	108.5		. 901	106	106	105.5	105	105		103.5	103	103	102.5	102	102	101	100.5	100.5	100	99.5	99.2	99.5	99.5	99.5	99.5	99.2	98.5
	Result No.	-	7	m	4	Ŋ	9	7	ω	σ.	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

P21860 homo sapien										Q13796 homo sapien
ERB3_HUMAN	NEST_HUMAN	GSR1_HUMAN	BIG1_HUMAN	ABF1_HUMAN	OTX_STRPU	HLX1_HUMAN	RGS3_MOUSE	IRS1_MOUSE	IRS1_HUMAN	APXL_HUMAN
٦ -		Ч	7	П	7	П	H	7	_	1
1342	1618	1509	1849	3703	371	488	568	1233	1242	1616
4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5
98.5	98.5	86	86	86	97.5	97.5	97.5	97.5	97.5	97.5
34	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 CSF1_MOUSE AC DOTAD DT 01-AP D
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                         332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MACROPHAGE COLONY STIMULATING FACTOR-1.
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
D -> G.
                                                                                                                                                    Broxmeyer H.E.;
"Cloning and characterization of the murine promoter for the colony-
stimulating factor-1-encoding gene.";
Gene 102:165-170(1991).
-!- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE
CYTCKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,
DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
OF THE BLOOD, THE GRANULCCYTES AND THE MONOCYTES-MACROPHAGES.
-!- FUNCTION: THIS CSF INDUCES MACROPHAGES.
-!- SUBUNIT: HOMODIMER, LINKED BY THREE DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQRTEGSS--LLPSELPL-----RIEDPGSAKQRP-----PRSTCQ-TLESTEQPNHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 RRLRNLIATAQAQNQQQTEGVKTEESEPLPSCPGSPPLPDDLLPLDCKNPNAPFQIRHSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PESDFYRGKGEPVTELSWHSCRQLLYQAVATILAHAGFDCANESVLETLTDVAHEYCLKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSQTNRSSFDLLPREFRLVEVHDPPLHQPSANKPKPPTMLDIPSEPCSLTIHTIQLIQHN
                                                                                                                                      Harrington M.A., Edenberg H.J., Saxman S.M., Pedigo L.M., Daub R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.7%; Score 123; DB 1; Length 552;
21.6%; Pred. No. 0.31;
Live 47; Mismatches 144; Indels 136;
CSF-1 gene. Post-transcriptional repression occurs in myogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DRL-----TEDSQPHPSAGGPVPGVEDIL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> A (IN REF. 1).
3886D72D70E770AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISSING (IN REF. 3).
A -> R (IN REF. 3).
AG -> PR (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1339753; Csfl.
Cytokine; Growth factor; Glycoprotein; Signal.
                                       Biochim. Biophys. Acta 1174:143-152(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S -> P
                                                                                              SPECIES-Mouse;
MEDLINE-91340149; PubMed=1874443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60648 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M21952; AAA37481.1; -...
EMBL; M2149; AAA37482.1; -...
EMBL; M15692; AAA37480.1; -...
EMBL; M44561; AAA03032.1; -...
EMBL; M81316; AAA19866.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X05010; CAA28660.1; -.
                                                                              SEQUENCE OF 1-13 FROM N.A.
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A26575; A26575
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552 AA;
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                    differentiation.";
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Ambine I., Hurt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
Bunham I., Hurt A.R., Collins J.E., Bruskiewich R., Babbage A.K.,
Bagguleg C., Balley J., Barlow K.F., Bates K.N., Beasley O.P.,
Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
Burrill W.D., Ductron J., Carder C., Collier R.E., Connor R.,
Conroy D., Corby N.R., Colle G.G., Cox A.V., Davis J., Dawson E.,
Bhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
A brank K.L., Fey J.M., Plenning K., French L., Garner A.B.,
A gilbert J.G.R., Goward M.E., Garfham D.V., Griffiths M.N.D., Hall C.,
A hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
A laird G.K., Langford C.F., Leversha M.A., Libyd C., Lloyd D.M.,
McClay J., Molaren S., McCurray A.A., Milne S.A., Mortimore B.J.C.T.,
A coll C.N., Parriet R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
Sodell C.N., Part H.K., Stuce C.D., Phillimore B.J.C.T.,
A coll C.N., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
Audin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
                                                                                                                                                                            241 DYHSYMLQISKQLSEEYERIVNPEKATEDAKPVKIKEEPVSDITFPVSEELEADLASGDQ 300
                                                                                                                                                                                                                                          : : | | : : | | | : : | | E----KTDGTSTLREDHQEPGSPHIATPNPQRVSNSATPVAQLLLPKSH-----SWGI 430
194 TKLLRFAVDREARLGQTPFP-----DVMEQVFHEVG----IGSVLSLQKFWQHRIK 240
                                                                                      ---IQAETDRPRALSASPFPKSTEDQKPVDITDRPLTEVNPMRPIGQT-----QNNTP 381
                                                                                                                                                                                                                                                                                                                                                                  301 SLPMGVL----GAQSERFPSNLEVEASPQASS---AEVNASPLWNLAHVKMEPQESEEGN 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S., Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D., Wambutt R., Korn B., Klein M., Poustka A.; Tampe J., Heubner D., analysis of 500 novel complete protein coding human convaint Genome Res. 11:422-435(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAC2_HUMAN STANDARD; PRT; 486 AA.
09UNF0; 09H0D3; 096HV9; 09NPN1; 095921; 09Y4V2;
15-UN-2002 (Rel. 41, Created)
15-UN-2002 (Rel. 41, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Protein kinase C and casein kinase substrate in neurons protein
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MEDLINE=99358785; PubMed=10431838;
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MEDLINE=21154917; PubMed=11230166;
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MEDLINE=20057165; Pubmed=10591208;
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HSSP; Q60631; 1GBQ

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Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L., Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N., Misoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J., Shimizu N., Shintani A., Shibuya K., Yoshizaki Y., Aoki W., Mitsuyama S., Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T., Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H., Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L., Phan S., Ang G., Wang Y., Wang Z., White J., Williapham D., Wu H., Yao Z., Lann M., Zhang G., Chissoe S., Murray J., Miller N., Minx P., Rulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S., Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J., Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R., Kang K., Kang K., Latreille P., Layman D., Ozersky P., Rohlfing T., Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peptand M., Kedra D., Seroussi E., Franson I., Tapia I., Bruder C.E., O'Brien K.P., Wilson R., Wilsinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell Sci. 13:4511-4521(2000).

Cell Sci. 13:4511-4521(2000).

Cell Sci. 13:4511-4521(2000).

Cell Sci. 13:4511-4521(2000).

Cell Sci. 14:4511-4521(2000).

Cell Sci. 15:4511-4521(2000).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The European IMAGE consortium for integrated molecular analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modregger J., Ritter B., Witter B., Paulsson M., Plomann M.; "All three PACSIN isoforms bind to endocytic proteins and inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Auffray C., Ansorge W., Ballabio A., Estivill X., Gibson K.,
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human gene transcripts.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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Nature 402:489-495(1999).
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EMBL, AL136845; CAB66779.1; --
EMBL, AL022476; CAB39175.1; --
EMBL, AL04978; CAB51395.1; --
EMBL, BC008037; AAH08037.1; --
EMBL, AL389984; CAB97538.1; --
GGENEW, HGNC:8571; PACSIN2.
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Genew; HGNC: { MIM; 604960;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : | | | : | | | : | | | : | | | : | | | : | | | | : | | | | : | | | : | | | : | | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 QLS-----EEYERIVNPEKATEDAKPVKIKEEPVSDITFPVSEELEADL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78;
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NCBI_TaxID=1423;
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MISSING (IN ISOFORM 2).
M -> I (IN DBSNP:2746984).
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V -> F (IN DBSNP:1062913).
                                                                                                                      PRINTS; PR00452; SH3DOMAIN.
ProDom; PR00665; SH3; 1.
SWART; SM00326; SH3; 1.
SWART; SM00326; SH3; 1.
PROSITE; PS50133; PC1; 1.
BROSITE; SF50002; SH3; 1.
Endocytosis; SH3 domain; Coiled coil; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       821DBEF65DAD1AA8 CRC64;
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L > F (IN REF. 1).

D -> N (IN REF. 1).

N -> I (IN REF. 1).

S -> F (IN REF. 1).

DDT -> EDI (IN REF. 1).
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15-JUN-2002 (Rel. 41, Last annotation update)
Stage VI sporulation protein D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.8%; Pred. No. 0.67;
tive 32; Mismatches
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                  InterPro; IPR001060; Cdc15_Fes_CIP4.
InterPro; IPR001452; SH3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55738 MW;
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Pfam; PF00018; SH3; 1.
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486 AA;
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A Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Borriss R., Bouster L., Brans A., Braun M., Brignell S.C., Bron S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Brouillet S., Brington J., Fabret C., Ferrari E., Foulger D.,

RA Britz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

RA Guiseppi G., Guy B.J., Haged K., Halech J., Harwood C.R., Henaut A.,

RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Kobayashi Y., Kooteter P., Koningstein G., Krogh S., Kumano M.,

R Kothayashi Y., Kooteter P., Mixuno M., Moestl D., Nakai S., Noback M.,

RA Noone D., O'Reilly M., Ogawa K., Ogiwra A., Oudega B., Park S.H.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescort R.,

RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,

RA Sato T., Scanlan E., Schleich S., Schroceter R., Scoffone F.,

Sckiguchi J., Sebowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,

RA Takeuchi M., Tamakoshi A., Tarakahashi H., Takemaru K.,

RA Takeuchi M., Tamakoshi A., Tarakahashi H., Wattzeneger T.,

RA Takeuchi M., Tamakoshi A., Tarakahashi H., Wattzeneger T.,

RA Takeuchi M., Tamakoshi A., Tarakahashi H., Wattseneger F.,

RA Takeuchi M., Tamakoshi A., Tarakahashi H., Wattseneger R.,

RA Takeuchi M., Wanbutt R., Wedler E., Wedler E., Wedler F., Vasumoto K., Yata K.,

RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vasumoto K., Yata K.,

RA Tosato V., Wanbutt R., Wedler E., Wedler H., Wasumoto K., Yata K.,

RA Toshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Ponkikawa H.F., Zumstein E.,

Rah Toshila K., Pasarotti M., Rah Toshikawa H.F., Zumstein E., Wedler W., Wasumoto K., Yasumoto K., Rah R., Rah R., Rah R., Rah R., Rah R., Rah 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bean Bioinformatics Institute. There are no restrictions on its non-profit institutions as long as its content is in no way
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DEVELOPMENTAL STAGE: EXPRESSION IS INITIATED AROUND THE SECOND HOUR OF SPORULATION AND CONTINUES THROUGHOUT DEVELOPMENT. MAY BE EXPRESSED PREDOMINANTLY IN THE MOTHER CELL.
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                                                      MEDLINE=98044033; PubMed=9384377;
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InterPro; IPR002482; LySM.
Pfam; PF01476; LySM; 1.
SMART; SM00257; LySM; 1.
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                     KQLSEEYERIVNPEKATED---AKPVKIKEEPVSDITFPVSEELEADLASGDQSLPMGVL 307
                                                                                                                                                                         211 PFPDV-MEQVFHEVGIGSV----LSLQK-----FWQHRIKDYHSYMLQ-----IS
                                                                                                            350 ADPALCQEEAEPDEALESVSEAALSIEDSRETASAVYMENDNADLHFHFNQKTSSEEASQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gansheroff L.J., Dollard C., Tan P., Winston F.; "The Saccharowyces cerevisiae SPT7 gene encodes a very acidic protein important for transcription in vivo."; Genetics 139:523-536(1995).
----FDCANESVL----ETLTDVAHEYCLKFTKLLRFAVDREARLGQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The bromodomain: a conserved sequence found in human, Drosophila and
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-!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR OF TY ELEMENTS AND POSSIBLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence analysis of a 31 kb DNA fragment from the right arm of Saccharomyces cerevisiae chromosome II.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Andre B., Cziepluch C., Hein C., Jauniaux J.C., Urrestarazu A., Vissers S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 463-523 FROM N.A.
MEDLINE-92285152; PubMed-1350857;
Haynes S.R., Dollard C., Winston F., Beck S., Trowsdale J.,
                                                                                                                                                                                                                          308 GAQSERFPSNLEVEASPQASSAEVNASPLWNLAHVKMEPQESEEGN 353
                                                                                                                                                                                                                                                               467 -- QSFQLPESSETERK-----ETDAVPRVAPAAETKEPQTKESDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                            PRT; 1332 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcriptional activator SPT7.
SPT7 OR YBR081C OR YBR0739.
Saccharomyces cerevisiae (Baker's yeast).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95229044; PubMed=7713415;
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                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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P35177;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSMSPNSNRTSRNSNSISSLAQQPPMSNYPQPSTYQYPGFHKTSSIPNSHSPIPPRSLTT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----PEKATEDAKPVKIKEEPVSDITFPVSEELEADLASGDQSL----PM--GVLG--A 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 GEIPISSSQTNRSSFDL--LPREFRLVEVHDPPLHQ------PSANKPKPPTMLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 PSE-----PCSLTIHTIQLIQHNRRLRNLIATAQAQNQQQTEGVKTEESEPLPSCPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 - PVTELSWHSCRQLLYQAVA - - - TILAHAGFDCANESVLETLTDVAHEYCLKFTKLLRFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         413 PRVTTTMWEDEKTLCYQVEANGISVVRRADNDWVNGTKL------LNVTKMTRGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | : | || : | || || 462 RDGILK-----AEKIRHYVKIGS-MHLKGVWIPFERALAIAQREKIADYLYPLFIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : | : | 512 DIQSVLKQNNPSNDSSSSSSSTGIKSISPRTYYQPINNYQNPNGPSNISAAQLTYSSMNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    572 NNKIIPNNSIPAVSTIAAGEKPLKKCTMPNSNQLEGHTITNLQTLSATMPMKQQLMGNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307 PTQGPTSQNGPLSYNLPQVGLL-------PPQQQQQVSPLYDGNSITPPVKPST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 PP-----LPDDLLPLDCKNPNAPFQ---IRHSDPESDFYRGKGE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VDREARLGQTPFPDVMEQVFHEVGIGSVLSLQKFW------QHRIKDY---;--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         310 QSERFPSNLEVEASPQASSAEVNASPLWNLAHVKMEPQESEEGNV------
   AND DEVELOPMENT. MAY INHIBIT THE SWITCH FROM UNICELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                        regulation; Nuclear protein; DNA-binding.
8 45 POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              F4E0F224BE84645F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 --HSYMLQIS------KQLSEE--YERIVN-----
              FILAMENTOUS GROWTH.
SUBCELLULAR LOCATION: Nuclear (Potential).
SIMILARITY: BELONGS TO THE EFG1/PHD1/STUA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67; Mismatches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---SGHGVLGSDVFEEPMSGM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.1%; Score 110.5; 18.8%; Pred. No. 3.6
                                                                                                                                                                                                                                                                                                                                                                                            POLY-TYR.
POLY-GLN.
POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                           POLY-TYR
                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :: | |: |: |: |: AEPVKESESSKSQVDGAGDVSNE 773
                                                                                                                                                                                                                                                                                 SGD; SOO(4618; SOK2.
InterPro; IPRO03163; Yeast_DNA_bind.
Pfam; PF02292; Yeast_DNA_bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85643 MW;
                                                                                                                                                                                                                                 EMBL; S80522; AAB35749.1; -. EMBL; Z49211; CAA89117.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                    TRANSFAC; T03616;
                                                                                                                                                                                                                                                                                                                                          Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Sim.
Matches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 AGFDCANESVLETLTDVAHEYCLKFTKLLRFAVDREARLGQTPFPDVMEQVFHEVGIGSV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          272 PVKIKEEPVSDIT----FPVSE-ELEADLASGDQSLPMGVLGAQSERFPSNLEVEASPQA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     940 NPNA-FLNNHIYNYTIIDDSLDI-----DPVSQLPTHDYKNNRELIWKFMHKNISKVAMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 LSLQKFWQHRIKDYHSYM------EKATEDAK
                                                                                                                                                                                                                                                                                                                                                                                                                           122 NPNAPFQIRH-----SDPESDFYRGKGEPVTELSWHSCR-----QLLYQAVATILAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lye G., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PLAYS A GENERAL REGULATORY ROLE IN THE CYCLIC AMP-
DEPRENDENT PROTEIN KINASE-STIMULATED (PKA) SIGNAL TRANSDUCTION
PATHWAY BY REGULATING THE EXPRESSION OF GENES IMPORTANT IN GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-96069395; PubMed-8524252;
Ward M.P., Gimeno C.J., Fink G.R., Garrett S.;
"SOK2 may regulate cyclic AMP-dependent protein kinase-stimulated growth and pseudohyphal development by repressing transcription.";
Mol. Cell. Biol. 15:6854-6863(1995).
                                                                                                                                                                                                                                              PROSITE; PS00633; BROMODOMAIN_1; 1.
PROSITE; PS50014; BROMODOMAIN_2; 1.
Transcription regulation; Nuclear protein; Activator; Bromodomain.
DOMAIN 458 5.28 BROMODOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327 SSAEVNASPLWNLAHVKMEPQESEEGNVSCHGVLGSDVFEEPMSGMSEAG 376
                                                                                                                                                                                                                                                                                                                                                          Length 1332;
                                                                                                                                                                                                                                                                                                                                                                                          96; Indels
                                                                                                                                                                                                                                                                                                                       083B63624669244F CRC64;
                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                         ć,
                                                                                                                                                                                                                                                                                                                                                       5.2%; Score 112.5;
11.4%; Pred. No. 5.3;
.ve 49; Mismatches
 email to license@isb-sib.ch)
                                                                                                                                                                       IPR001487; Bromodomain.
                                                                                                                                                                                                                                                                                                                    152616 MW;
                               EMBL, L22537; AAC37424.1; --
EMBL, X76294 (CA53940.1; --
EMBL, 235950; CAA85026.1; --
EMBL, M87651; AAA35087.1; --
PIR, S41552; S41552.
HSSP, Q92831; 1B91.
TRANSFRG; T04835; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOK2 protein.
SOK2 OR YMR016C OR YM9711.03C.
                                                                                                                                                                                                              PRINTS; PR00503; BROMODOMAIN.
SMART; SM00297; BROMO; 1.
                                                                                                                                                                                               Pfam; PF00439; bromodomain;
                                                                                                                                                                                                                                                                                                                                                                       21.4%;
                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 21.49
Matches 62; Conservative
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                                                                                                                                                                                                                                                                                                                    SEQUENCE 1332 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4932;
                                                                                                                                                       SGD; S0000285;
InterPro; IPR0
   an
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P53438;
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send
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SOK2_YEAST
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24;

66C17ECCC767E0E7 CRC64;

486 AA; 55833 MW;

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SEQUENCE
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                                          Matches
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                                                                                                                                                                                                                                                                                                                                     STRAIN-C57BL/6 x DBA;
MEDLINE-99358785; PubMed-10431838;
Ritter B., Modregger J., Paulsson M., Plomann M.;
"PACSIN 2, a novel member of the PACSIN family of cytoplasmic adapter proceins.";
FEBS Lett. 454:356-362(1999).
                                       15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protein kinase C and casein kinase substrate in neurons protein 2.
                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                         Modregger J., Ritter B., Witter B., Paulsson M., Plomann M.; "All three PACSIN isoforms bind to endocytic proteins and inhibit
                                                                                                                                                                                                                                                                 Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50133; FCH; 1.
PROSITE; PS50002; SH3; 1.
Endocytosis; SH3 domain; Coiled coil; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SH3.
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                              (PKC) (By similarity).
-!- SIMILARITY: BELONGS TO THE PACSIN FAMILY.
-!- SIMILARITY: CONTAINS 1 FCH DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                    486 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BC023502; AAH23502.1; -. HSSP; P29555; ISEM. MGD; MGI:1345153; Pacsin2. InterPro; IPR001060; Cdc15_Fes_CIP4. InterPro; IPR001452; SH3.
                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF128535; AAD41780.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS: PR00452; SH3DOMAIN.
ProDom; PD000066; SH3; 1.
SMART; SM00055; FCH; 1.
SMART; SM00326; SH3; 1.
                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00611; FCH; 1.
Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE-Mammary gland;
                                                                                           musculus (Mouse).
                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                               PubMed=11082044;
                                                                                                                                                                                                                                                       Strausberg R.;
                                                                                                                                                                                                                                                                                                                              endocytosis.
                    PAC2_MOUSE
                                                                                   PACSIN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
DOMAIN
                               09WVE8
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13;
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                                                                                                                                                                                                 134 AEDGFRKAQKPWAKKLKEVEAAKKAHHTACKEEKL---AISREANSKADPSLNPEQLKKL 190
                                                                                                                                                                                                                                                                                                                                                                                                DYHSYMLQISKQLS------EEYERIVNPEKATEDAKPVKIKEEPVSDITFPVSE 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 FFREVLLEVQKHLDLSNVASYKTIYRELEQSIKAADAVEDLRWFRANHGPGMAMNWPQFE 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSAEVNASPLWNLAHVKMEPQESEEGNVSGHGVLGSDVFEEP-----MSGMSEAGIPQ 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353 OSTOLOSS-----YNPFEDEDDT-----GSSISEKEDIKAKNVSSYEKTQTYPT 396
                                                                                                                                                                                                                                                                 -----RLGQT--PFPDVMEQVFHEVGIGSVLSLQKFWQHRIK
                                                                                                                                                                                                                                                                                                                                191 QDKIEKCKQDVLKTKDKYEKSLKELDQTTPQYMENMEQVFEQ------CQQFEEKRLR
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STRAIN-S288C / AB972;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,
Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,
Wilson R., Waterston R.,
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FIBRONECTIN TYPE III DOMAIN.
MEDLINE-97148176; PubMed-8994808;
Bateman A., Chothia C.;
"Fibronectin type III domains in yeast detected by a hidden Markov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                  94; Indels 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: INVOLVED IN CHITIN SYNTHESIS AND ALSO REQUIRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97265380; Pubmed-9111317; Santos B., Duran A., Valdivieso M.H.; "CHS5, a gene involved in chitin synthesis and mating in cancharamence caredisiae.":
                                                                                                                                  167 AHAGFDCANESVLETLTDV----AHEYCLKFTKLLRFAVDREA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAX-2000 (Rel. 39, Last annotation update)
Chitin biosynthesis protein CHS5 (CAL3 protein).
CHS5 OR CAL3 OR YLR330W OR L8543.18.
DB 1;
5.0%; Score 109; DB 21.4%; Pred. No. 2.4; tive 35; Mismatches
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Mol. Cell. Biol. 17:2485-2496(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  397 DWSDDESNNPFSSTDANGDSNP 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      380 SPDDSDSSYGSHSTDSLMGSSP 401
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                                                                  69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELEADL-----
   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-GRF88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHS5_YEAST
Q12114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MATING
                                                                                                                                                                                                                                                                 206
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228
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15-JUN-2002 (Rel. 41, Last annotation update)
Golgi-specific brefeldin A-resistance guanine nucleotide exchange
factor 1 (BFA-resistant GEF 1).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Best Local Similarity 20.5%; Pred. No. 4;
Matches 76; Conservative 53; Mismatches 159; Indels
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FA92741B862814C2 CRC64;
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MEDLINE=99047539; PubMed=9828135;
                                                                                                                                                                                                EMBL; 249198; CAA89059.1; --
EMBL; U20618; AAB64526.1; --
SGD; SO0040322; CHS5.
InterPro: IPR001357; BRCT.
InterPro: IPR003961; FN_III.
Pfam; PF00041; fn3; 1.
SMART; SM00292; BRCT; 1.
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73638 MW;
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Q92538;
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   Scherer S.W., Melancon P.; expressed gene of the sec7 domain family
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                                                                                                                                                                                                                                                        Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y., Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
Prediction of the coding sequences of unidentified human genes. VI.
The coding sequences of 80 new genes (KIAAO201-KIAAO280) deduced by analysis of cDNA clones from cell line KG-1 and brain.";
DNA Res. 3:321-329(1996).
THE ACTIVATION OF ARFS THROUGH REPLACEMENT OF GDP WITH GTP (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENZYME REGULATION: INHIBITED BY BREFELDIN A (BY SIMILARITY). TISSUE SPECIFICITY: UBIQUITOUS.
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DOMAIN 696 884 SEC7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF068755; AAD15903.1; -.
                                                                                                                                                          SEQUENCE OF 169-1859 FROM N.A.
Mansour S.J., Herbrick J.-A., "Human GBF1 is a ubiquitously
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D87435; BAA13379.1;
HSSP; Q99418; 1PBV.
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                                                            mapping to 10q24.";
Genomics 54:323-327(1998)
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MIM; 603698; -.
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Matches 80; Conserv
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272 Q-----NL-----HDESLSTSPHGALHQHVTDIQLHILKNRMYGCDSVKQPRNIE 316
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Matches 72; Conserv
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                      6-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 605358;
                                                                                            T2AY_HUMAN
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                                                                                                           Q9UNN4;
                                                                                T2AY_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 /
                                                                                                                                                                                                                                                                                                                                                                                            -1- PTM: Substrate of transglutaminase. Specific glutamines or lysines
                                                                                                                                                                                                                                                      Djian P., Green H.;
"Involucrin gene of tarsioids and other primates: alternatives in evolution of the segment of repeats."

Proc. Natl. Acad. Sci. U.S.A. 88:5321-5325(1991).

- FUNCTION: Part of the insoluble cornified cell envelope (CE) of stratified squamous epithelia.

-! SUBCELLULAR LOCATION: Cyroplasmic. Constituent of the scaffolding of the cornified envelope.

-! TISSUE SPECIFICITY: Keratinocytes of epidermis and other stratified squamous epithelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNLIATAQAQNQQQTEGVKTEESEPLPSCPGSPPLPDDLLPLDCKN-PN---APFQIRHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GELLKTVPPPANTQQDQMKQPTPSPAPCQKGPSELPVEKHPAPVKQVPEQECEPQQQDHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPESDFYRGKGEPVTELSWHSCRQLLYQAVATILAHAGFDCANESVLETLTDVAHEYCLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTKLLRFAVDREARLGQTPFPDVMEQVFHEVGIGSVLSLQKFWQHRIKDYHSYMLQISKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGKQQQKTQEQEVHLGKQQ-QELQEQEVH-----LEKQLQEP-QEVH-----LEKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSEEYERIVNPEKATEDAKPV----KIKEEPVSDITFPVSEELEADLASGDQSLPMGV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOBOE---VHLEKOLOEPEPELNLGKOOOEP------OEOEAYLGKOOOELPEPODP
                                                                                                                                                                                                                                                                                                                                                                                                            are cross-linked to keratins, desmoplakin and to inter involucrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPELOLGRKOOEP-OEOEVHPGKO--QQKPQEQEAHLG-----KKQEPQGQEVH----
                                                                                                                                               Tarsius-bancanus (Western tarsier) (Horsfield's tarsier).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Tarsii; Tarsiidae; Tarsius.
NCBI_TaxID=9477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.9%; Score 106; DB 1; Length 387; 23.0%; Pred. No. 2.8; ve 37; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | | | : | | | : | | | : | | ELHLGKQQQE-----LHLGKQQQESQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45077 MW; 146BAC2E490AA805 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE INVOLUCRIN FAMILY.
                                                                           (Rel. 21, Created)
(Rel. 21, Last sequence update)
(Rel. 41, Last annotation update)
                                                   387 AA.
                                                   PRT;
                                                                                                                                                                                                                                             MEDLINE-91271381; PubMed-1905021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.0%; Pic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002360; Involucrin.
PROSITE; PS00795; INVOLUCRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M65124; AAA36960.1; -
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                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Keratinization; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A43704; A43704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 76; Conserv
                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                            molecules
                                                                                                                                                                                                                                TISSUE-Liver
                                                                             01-MAR-1992
01-MAR-1992
                                                                                                        15-JUN-2002
                                                                                                                      Involucrin.
                                                   TARBA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Upadhyaya A.B., Lee S.H., DeJong J.;
"Identification of a general transcription factor TFIIA(alpha)/(beta)
homolog selectively expressed in testis.";
J. Biol. Chem. 274:18040-18048(1999).
-!- FUNCTION: MAY FUNCTION AS A TESTIS SPECIFIC TRANSCRIPTION FACTOR.
BINDS DNA IN CONJUNCTION WITH GTF2A2 AND TBP (THE TATA-BINDING
PROTEIN) AND TOGETHER WITH GTF2A2, ALLOWS MRNA TRANSCRIPTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 FQQLGQPSVI-----QTSVPQLNPWSLQATTEKSQRIETVLQ-QPAILPSGPVDRKHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 KVLQSKATEDFFRNSIQSPLFTLQLPHSLHQTLQSSTASLVIPAGRTLPSFTTAELGTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --VLETLTDVAHEYCLKFTKLLRFAVDREARLGQTPFPDVMEQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 SSANFTFPGYPIHVPAGVTLQTVS--GHLYKVNVPIMV---TETSGRAGILQHP--IQQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FHEVGIGSVLSLQKFWQHRIKDYHSYMLQISKQLSEEYERIVNPEKATEDAKPVKIK--E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278 EPVSDITFPVSEE----LEADLASGDQ----SLPMGVLGAQSERFPSNLEVEASPQASSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84;
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SEQUENCE 478 AA; 52445 MW; 0EF012A79CD17619 CRC64;
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                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) TFIIA-alpha and beta like factor (ALF).
                                                                 254 -- EQELHLRKLQQVPQEPQDQELHLGKQQQE 282
364 VFEEPMSGMSEAGIPQSPDDSDSSYGSHSTD 394
                                                                                                                                                                                                                                                      Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.9%; Score 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Testis;
MEDLINE-99292779; PubMed-10364255;
                                                                                                                                                                                                                                                                                                               (Rel. 40, Created)
(Rel. 40, Last seq
(Rel. 41, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR004855; TFIIA.
Pfam; PF03153; TFIIA; 1.
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                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                   Kordell E., Lambert S., Bennett V.;
Rordell E., Lambert S., Bennett V.;
Rankyring. A new ankyrin gene with neural-specific isoforms localized at the axonal initial segment and node of Ranvier.";
J. Biol. Chem. 270:325-2359(1995).
I- FUNCTION: Membrane-cytoskeleton linker.
I- ALTERNATIVE PRODUCTS: A number of isoforms are produced by alternative splicing.
I- TISSUE SPECIFICITY: Expressed in brain and other tissues.
I- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS5008; ANK_REPEAT; 21.
PROSITE; PS50297; ANK_REP_REGION; 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
Cytoskeleton; Alternative splicing; Repeat; ANK repeat.
REPEAT 106 135 ANK 2.
ANK 2.
                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ankyrin 3 (Ank-3) (Ankyrin G).
                                                                                                                                                               4377 AA.
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                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain stem;
MEDLINE=95138209; PubMed=7836469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANK
ANK
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                                                                               1021 EPSNIPVSEKDSNS 1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00023; ank; 24.
Pfam; PF00131; death; 1.
Pfam; PF00701; 2U5; 1.
PRINTS; PR01415; ANKTRIN.
SMART; SM00248; ANK; 21.
SMART; SM00005; DEATH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002110; ANK.
InterPro; IPR000488; Death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000906; ZU5.
                                                                                                                                                               STANDARD;
                                                   373 SEAGIPQSPDDSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:494; ANK3.
      -IN-----0 926
                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 600465;
                                                                                                                                                               ANK3_HUMAN
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REPEAT
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ANK3_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GSDVFEEPMSGM 372
                                                                                                                                                                                                                                                                                                                                                 Upadhyaya A.B., Lee S.H., DeJong J.;
"Identification of a general transcription factor TFIIAalpha/beta
homolog selectively expressed in testis.";
J. Biol. Chem. 274:18040-18048(1999).
-!- SUBCELLUAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN TESTIS, HEART, PLACENTA,
KIDNEY, PROSTATE AND UTERUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSANFTFPGYPIHVPAGVTLQTVS--GHLYKVNVPIMV---TETSGRAGILQHP--IQQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       916 NATSDILVSPGNEHKIVPEALLCHQESSHYISLPGVVFSPQVSQTNSDVESVLSGSASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 FHEVGIGSVLSLQKFWQHRIKDYHSYMLQISKQLSEEYERIVNPEKATEDAKPVKIK--E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPVSDITFPVSEE----LEADLASGDQ----SLPMGVLGAQSERFPSNLEVEASPQASSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 ES------VLETLTDVAHEYCLKFTKLLRFAVDREARLGQTPFPDVMEQV
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IN THE N-TERMINUS TO MEMBERS OF THE ADAPTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1182 AA; 132037 MW; 22AD66366D21C371 CRC64;
                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Stoned B-TFIIA-alpha and beta like factor (SALF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330 EVNASPLWNLAHVKMEPQESEEGNVSGHGVL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001392; Clathrn_med.
InterPro; IPR004855; TFIIA.
Pfam; PF00928; Adap_comp_sub; 1.
Transcription regulation; Nuclear protein.
DOMAIN 44 150 PRO/SER/THR-RICH.
                                                                                                             1182 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
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COMPLEXES MEDIUM SUBUNITS FAMILY
                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                    MEDLINE=99292779; PubMed=10364255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF026169; AAD39617.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.9%;
                   : || | ||:|
317 EPSNIPVSEKDSNS 330
373 SEAGIPQSPDDSDS 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72; Conservative
                                                                                                            STANDARD;
                                                                                                                                                                                                                          (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P32773; 1YTF
                                                                                                                                                                                                                                                                                                                     TISSUE=Placenta;
                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 605357;
                                                                                                        T2AZ_HUMAN
Q9Y6Q2;
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                                                                                              T2AZ_HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifised and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and 4/Db; are produced by alternative splicing.
--- TISSUE SPECIFICITY: Ubiquitously expressed. Isoforms 1 and 3 are expressed in PC12 cell line and heart, whereas isoforms 2 and 4 are seen in most tissues examined with higher levels of expression
                                                                                                                                                                                                                                                                                                                                             in muscle, testis and brain. PTM: Phosphorylated by casein kinase {\tt C}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --RLGQT--PFPDVMEQVFHEVGIGSVLSLQKFWQHRIK
                                     Qualmann B., Keily R.B.; "Syndapin isoforms participate in receptor-mediated endocytosis and
                                                                                                                                                                                                                                                                           -!- ALTERNATIVE PRODUCTS: 4 isoforms; 1/aa (shown here), 2/ab, 3/ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COILED COIL (POTENTIAL).
MISSING (IN ISOFORM 3 AND ISOFORM 4).
MISSING (IN ISOFORM 2 AND ISOFORM 4).
M251NG (IN ISOFOFF 2 CRC64;
                                                                                                                                     Modregger J., Ritter B., Witter B., Paulsson M., Plomann M.; "All three PACSIN isoforms bind to endocytic proteins and inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.8%; Score 105; DB 1; Length 488;
2.5%; Pred. No. 4.5;
.ve 33; Mismatches 103; Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AHAGFDCANESVLETLTDV - - - - AHEYCLKFTKLLRFAVDREA - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coiled coil; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
STRAIN-Sprague-Dawley; TISSUE-Brain;
MEDLINE-20171438; PubMed-10704453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF139494; AAF22213.1; --
EMBL; AF139494; AAF22214.1; --
HSSP; P29355; 1SEM.
INCEPPRO; IPR001060; Cdc15_Fes_CIP4.
INCEPPRO; IPR001452; SH3.
Pfam; PF00011; PCH; 1.
Pfam; PF000118; SH3; 1.
PRINTS; PR00452; SH3DOMAIN.
SMART; SM00055; FCH; 1.
SMART; SM00326; SH3; 1.
                                                                    actin organization.";
J. Cell Biol. 148:1047-1062(2000)
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22.5%; Pr.
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55978
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PROSITE; PS50002; SH3; 1.
Endocytosis; SH3 domain;
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488 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 71; Conserv
                                                                                                                                                                                                                                                                distribution.
                                                                                                                      PubMed=11082044;
                                                                                                                                                                 endocytosis.'
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SEQUENCE
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                                                                                                           FUNCTION
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                                                                                                                                                                                                                                                                                                                                                          2368 GDINLKDFLPEKHDAFPCSEEQGQQEEEELTAEES--LPSY------LESSRVN 2413
                                                                                                                                                                                                                                                                                           2585 EEKLTEVSOFFRDKTEKLNDELQSPEKKARPKNGKEYSSOSPTSSSPEKVLLTELLASND 2644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2705 QSGFQLKQSKLSSIRLKFEQGTHAKSKDMSQEDRKSDGQSRI-----PVKKIQESKLP 2757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2525 NGVGKVSKDEHFDKVTVLHYSGNVSSPKHAMWMRFTEDRLDRGREKLIYEDRVDRTVKEA 2584
                                                                                                                                                                                                                                                                                                                                                                                     125 APF-QIRHSDPES-----DFYRGKGEPVTELSWHS------CRQLLYQAVATILA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                           | :: | | :: |: :| | SEKLDVSHSDTEESVTDHAGPPSSELQ----GSDKRSREKIATAPKKEILSKIYKDVSE
                                                                                                                                                                                                                                                                                                                                HNRRLRNLI - - - - - ATAQAQNQQQTEGVKTEESEPLPSCPGSPPLPDDLLPLDCKNPN
                                                                                                                                                                                                                                                                                                                                                                                                               2414 TPVSQEEDSRPSSAQLISDDSYK----TLKLLSQHSIEYHDDELSELRGESYRFAEKMLL
                                                                                                                                                                                                                                                                                                                                                                                                                                           168 HAGFDCANESVLETLTDVAHEYÇLKFTKLLRFAVDREAR--LGQTPFPDVMEQVFHEV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               224 -GIGSVLSLQKFWQHRIKDY-----HSYMLQISK-QLSEEYERIVNPEKATEDAKPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIKEEPVS----DITFPVSEELEAD-----LASGD
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                                                                                                                                                                                                                                                                          SSSQTNRSSFDLLPREFRLVEVHDPPLHQPSANKPKPPTMLDIPSEP-CSLTIHTIQLIQ
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
[1]
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Synaptic dynamin-associated protein II) (Syndapin 2) (Syndapin-II)
(SdpII).
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protein kinase C and casein kinase substrate in neurons 2 protein
                                                                                                                                                                                                                                                 Indels 161;
                                                                                                                                                                                                                     Length 4377;
                                                                                                                                                                                           F42379E55768B684 CRC64;
                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                169;
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                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                   Score 105.5;
Pred. No. 81;
                                                                                                                                                   ANK 23.
SER-RICH.
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                                                                                                                                                                               DEATH
                                      ANK
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                                                                                                                                                                                         480399 MW;
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18.1%;
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                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                   Similarity
91;
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                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                               -----TEDAKPVKIKEEPVSDITFPV
                                                           ---LKFTKLLRFAVDREARLGQTPFPDVMEQVFHE----VGIGSVLSLQKFWQHRIKDY
                                                                                                                                                                                       483 ISKEKFMEHIITYHEFAENPGLIDNPNLVIRIYNRYYNWALAAPMILSLQVFQK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDILNE-973131507; PubMed-975705; Kohlhase J., Schuh R., Dowe G., Kuehnlein R.P., Jaeckle H., Schlase J., Schulz-Schaeffer W., Kretzschmar H.A., Koehler A., Mueller U., Raab-Vetter M., Burkhardt E., Engel W., Stick R., Isolation, characterization, and organ-specific expression of two novel human zinc finger genes related to the Drosophila gene spalt.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marlin S., Blanchard S., Lacombe D., Denoyelle F., Alessandri J.-L., Calzolari E., Drouin-Garraud V., Ferraz F.G., Fourmaintraux A., Philip N., Toublanc J.E., Petit C.; "Townes-Brocks syndrome: detection of a SALLI mutation hot spot and evidence for a position effect in one patient."; Hum. Mutat. 14:377-386(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular analysis of SALL1 mutations in Townes-Brocks Syndrome."; Am. J. Hum. Genet. 64:435-445(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-26 FROM N.A., DISEASE, AND VARIANTS SER-164 DEL AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kohlhase J., Wischermann A., Reichenbach H., Froster U., Engel W. "Mutations in the SALLI putative transcription factor gene cause Townes-Brocks syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kohlhase J., Taschner P.E.M., Burfeind P., Pasche B., Newman B., Blanck C., Breuning M.H., ten Kate L.P., Masawinkel-Mooy P., Mitulla B., Seidel J., Kirkpatrick S.J., Pauli R.M., Wargowski D beviiendt K., Proesmans W., Gabrielli O., Coppa G.V., Wesby-van Swaay E., Trembath R.C., Schinzel A.A., Reardon W., Seemanova E., Engel W. Trembath R.C., Schinzel A.A., Reardon W., Molecular analysis of SALLI mutations in Townes-Brocks Syndrome
                            139 YRGKGEPVTELSWHSCRQLLYQAVATILAHAGFDCANESVLETLTDVAHEYC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAL1_HUMAN STANDARD, PRT; 1324 AA.
Q9NSC2; Q9NSC3; Q998B1; Q991R0;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Sal-like protein 1 (Zinc finger protein SALL1) (Spalt-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                          324
                                                                                                                                                                                                                                                                                                                                                                                         592 KEPAGARPAENDSSSDEG----SQELEESITVDPIP
                                                                                                                                                                                                                                                                                                                                                       SEELEADLASGDQSLPMGVLGAQSERFPSNLEVEASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 313-345 FROM N.A., AND DISEASE. MEDLINE-98085876; PubMed-9425907;
                                                                                                                                                                                                                                               243 HSYMLQISKQLSEEYERIVNPEKA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20004537; PubMed=10533063;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99138656; PubMed=9973281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcription factor 1) (HSall)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                 LSGSQSP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SALL1 OR SAL1
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SEOUENCE OF
                                                                              438
                                                                                                                                                                                                                                                                                                     537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAL1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
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|:| : |::
-----CQOFEEKRIR 242
                                                                                                                                                                                                                                                                                                                                 KPKPPTMLDIPSEPCSLTIHTIQLIQ --- HNRRLRNLIATAQAQNQQQTEGVKTEESEPL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSCPGSPPL-----PDDLLPLDCK--NPNAP---FQIRHSD----PESDF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYHSYMLQISKQLS-------EEYERIVNPEKATEDAKPVKIKEEPVSDITFP--V
                                                                                                                              243 FFREVLLEVQKHLDLSNVASYKGIYRELEQSIKAADAVEDLRWFRANHGPGMAMNWPQFE
                                                                                                                                                                                    288 SEELEADL------ASGDQSLPMGVLGAQS--ERFPSNLEVEASPQASSAEVNA
                                                                                                                                                                                                                                       303 DEEWSADLNRTLSRREKKKAADGVTLTGINQTGDQSGQNKPSSNLSVPSNP-AQSTQLQS
                                                                                                                                                                                                                                                                                            SPLWNLAHVKMEPQESEEGNVSGHGVLGSDVFEEP-----MSGMSEAGIPQSPDDSDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KPKPRALGTQMSDPTSVA----ELLEPPLESTQISSMLDADHLPNAALAEA----PSESK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nagase T., Seki N., Ishikawa K.-İ., Ohira M., Kawarabayasi Y., Ohara O., Tanaka A., Kotani H., Miyalima N., Nomura N.;
"Prediction of the coding sequences of unidentified human genes. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced lanalysis of cuba A.clones from cell line KG-1 and brain.";
DNA Res. 3:321-329(1996).
-I. SIMILARITY: TO HUMAN KIAA0188 AND YEAST SMP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGNC:14450; LPIN2.
etical protein.
CE 896 AA; 99399 MW; 080113FCCA533272 CRC64;
QDKIEKCKQDVLKTKDKYEKALKELDQTTPQYMENMEQVFEQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein KIAA0249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 896 AA.
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Pred. No. 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Bone marrow;
MEDLINE=97191544; PubMed=9039502;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          406 NNPFSSTDANGDSNP 420
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                                                                                                                                                                                                                                                                                                                                                                                                       387 SYGSHSTDSLMGSSP 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 4.8%;
Similarity 19.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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Best Local Simi
Matches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y249_HUMAN
Q92539;
                                                                                                                                                                                                                                                                                               334
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                                                                                                                                                                                                                                                                                                                                                (TBS); a rate, autosomal dominant malformation syndrome with a combination of imperforate anus, triphalangeal and supernumerary thumbs, malformed ears and sensorineural hearing loss.

-!- DISEASE: Defects in SALI are in rare cases associated with hemifacial microsomia (HFM) or Goldenhar syndrome; a common birth defect involving first and second branchial arch derivatives. The highly variable phenotype shows in addition to craniofacial anomalies cardiac, vertebral, and central nervous system defects.
-!- DISEASE: Defects in SALI are associated with branchio-oto-renal (BOR) syndrome, an autosomal dominant disorder manifested by various combinations of preauricular pits, branchial fistulae or cysts, lacrimal duct stenosis, hearing loss, structural defects of the outer, middle, or inner ear, and renal dysplasia. Associated defects include asthenic habitus, long narrow facies, constricted palate, deep overbite, and myopia. Hearing loss may be due to mondini type cochlear defect and stapes fixation.
-!- SIMILARITY: BELONGS TO THE SAL FAMILY OF C2H2-TYPE ZINC-FINGER
                                                                                                                       SUBUNIT: Interacts with HDAC1, HDAC2, RBBP4, RBPP7, MTA1 and MTA2 (MS similarity). Probably associates with NuRD histone deacetylase
                                                                                                                                                              COMPLEX (HDAC).
SUBCELLUIAR LOCATION: Nuclear (By similarity).
SUBCELLUIAR LOCATION: Nuclear (By similarity).
TISSUE SPECIFICITY: Highest levels in kidney. Lower levels in adult brain (enriched in corpus callosum, lower expression in substantia nigra) and liver.
DEVELOPMENTAL STAGE: In fetal brain exclusively in neurons of the subependymal region of hypothalamus lateral to the third
                                                                                                                                                                                                                                                                                                                                 DISEASE: Defects in SALL1 are the cause of Townes-Brocks syndrome
                                                           fed. Genet. 37:458-460(2000).
FUNCTION: Transcriptional repressor involved in organogenesis (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ranscription regulation; Repressor; DNA-binding; Nuclear protein;
Engels S., Kohlhase J., McGaughran J.;
"A SALL1 mutation causes a branchlo-oto-renal syndrome-like
                                                                                                                          SUBUNIT: Interacts with HDAC1, HDAC2, RBBP4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Metal-binding; Repeat; Polymorphism
49 471 C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD000003; Znf-C2H2; 1.
PROSITE: PS00028; ZINC_FINGER_C2H2_1; 9.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
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C2H2-TYPE.
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C2H2-TYPE.
C2H2-TYPE.
POLY-SER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000822; Znf_C2H2.
Pfam; PF00096; zf-C2H2; 10.
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                                                                                                        similarity).
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                                                                                                                                                                                                                                                                                                                                              ----- SSSSSSSGGGSS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 RFPSNLEVEASPQASSAEVNASPLWNLAHVKMEPQESEEGNVSGHGVLGSDVFEEPMSGM 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 ------ASQSASISGVKQLPPIQL-----PQSS-----SGNTIIPSNSGSSPNMNI 343
                                                                                                                                                                                                                                                                                    213 EARCGGASGGKLAVPALMEQ-----LLALQ---QQQI-----HQLQLIEQIRHQIL 255
                                                                                                                                                                                                                                                                    34 VHDPPLHQPSANKPKPPTMLDIPSEPCSLTIHTI-----QLIQHN--RRLRNLIATAQA 85
                                                                                                                                                                                                                                                                                                                                                                                     166 STGTS-----AITTSLPQLGDLTTLGNFSVINSNVIIEN---LQSTKVAVAQFSQ
                                                                                                                                                                                                                                                                                                                                                                        146 VTELSWHSCRQLLYQAVATILAHAG--FDCANESVLETLTDVAHEYCLKFTKLLRFAVDR
                                                                                                                                                                                                                                                                                                                                                                                                                        EARL-----GQTPFPDVMEQVFHEVGIGSVLSLQKFWQHRIKDYHSYMLQISKQLSEEYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                               4.8%; Score 103.2;
22.0%; Pred. No. 22;
*ive 53; Mismatches 140; Indels 115;
                                                                                                                                                                               CAB41399).
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CBE787847A96D8AA CRC64;
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/FTId=VAR_013159.
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                                                                                                                                                                                                                                                                                                                                              132 ANK --- SGSGTSSGSHSSTAPSS------
                                     POLY-SER.
                                                                          SS
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Best Local Similarity
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                                                                                                                                                                                           SEQUENCE
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us-09-857-308-1.rpr

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

. OM protein - protein search, using sw model

Run on:

July 18, 2003, 09:48:28 ; Search time 45.128 Seconds (without alignments) 881.929 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-857-308-1 2175 1 MNLQRYWGEIPISSSQINRS......SLMGSSPVFNQRCKKRMRKI 414

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	,		hypothetical prote	macrophage colony-	colony-stimulating	hypothetical prote	spore coat assembl	probable transcrip	hypothetical prote		protein -	se	hypothetical prote			hypothetical prote				hypothetical prote	ankyrin 3, long sp	205K microtubule-a	protein F10G7.9 [i	ankyrin-related pr	meiotic recombinat	hypothetical prote	coaqulation factor	natural killer cel	excinuclease ABC s	prot
SUMMARIES	ID	3000VE	140006	A82255	A31401	S35703	T33152	A69716	S41552	T28736	S54016	S53407	T34021	T26216	T26215	A43704	T20773	T20771	T20774	T15348	T25111	A55575	A36685	A88131	D57282	S72229	T21122	KFHU5	A47328	H86502	T24365
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d	Query Match			n.	5.7	5.7	5.6	5.4	5.2	5.1	5.1	5.0	5.0	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.8	4.8	4.8	4.8	4.8	4.8	4.7	4.7	4.7
	Score	' -	7.7	07T	123	123	121.5	117	112.5	112	110.5	108.5	108.5	107	107	106	106	106	106	106	105.5	105.5	105	104.5	104.5	104	103.5	103.5	103	103	102.5
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hypothetical prote versican precursor	hypothetical prote hypothetical prote	apolipoprotein E p V-type ATPase, sub	serine/threoine pr	hypothetical prote	hypothetical prote ervthrocyte bindin	fxbC protein - Myc	peptide synthetase	IMP-E2 protein pre	homeotic protein H	pyruvate decarboxy	neurabin - rat
T26656 T42389	T27388 H96597	A28792 E70111	T18532	A84470	AC1194 T28652	T14182	T14164	A37351	A39621	DCZYPZ	T43275
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30	32 33	34 35	36	37	20 G 20 G	40	41	42	43	44	45

## ALIGNMENTS

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A; Regerence number: JNU294; MULD:91340149; PAID:18/4443
A; Accession: JNU294
A; Molecule type: DNN
A; Residues: 1-13 cHAR>
A; Accession: JNU294
A; Molecule type: DNN
A; Residues: 1-13 cHAR>
A; Cross-references: GB:M81316; GB:M61708; NID:g192802; PIDN:AAA19866.1; PID:g192803
A; Cross-references: GB:M81316; GB:M61708; NID:g192802; PIDN:AAA19866.1; PID:g192803
A; Title: Nucleotide sequence of a cDNA encoding murine CSF-1 (macrophage-CSF).
A; Reference number: A25675
A; Molecule type: mRNA
A; Molecule type: MRNA
A; Molecule type: MRNA
A; Residues: 1-5, A', 247-552 cDEL>
A; Molecule type: MRNA
A; Residues: 1-5, A', 247-552 cDEL>
A; Molecule type: MRNA
A; Reference number: A23166; MUID:8542709; PMID:3925458
A; Accession: A23166
A; Molecule type: MRNA
A; Residues: 33-39, CC', A-57 cBEN>
B; Rajavashisth, T.B.; Eng, R.; Shadduck, R.K.; Waheed, A.; Ben-Avram, C.M.; Shively,
B; Rajavashisth, T.B.; Eng, R.; Shadduck, R.K.; Waheed, A.; Ben-Avram, C.M.; Shively,
B; Rajavashisth, T.B.; Eng, R.; Shadduck, R.K.; Waheed, A.; Ben-Avram, C.M.; Shively,
B; Rajavashisth, T.B.; Eng, R.; Shadduck, R.K.; Waheed, A.; Ben-Avram, C.M.; Shively,
B; Rajavashisth, T.B.; Eng, R.; Shadduck, R.K.; Waheed, A.; Ben-Avram, C.M.; Shively,
B; Rajavashisth, T.B.; Eng, R.; Shadduck, R.K.; Waheed, A.; Ben-Avram, C.M.; Shively,
B; Reference number: A25883; MUID:87147232; PMID:3493488
A; Molecule type: mRNA
A; Reference General Status greating factor
C; Keywords: GB:M15829; NUID:97192800; PIDN:AAA37480.1; PID:9192801
C; Superfamily: macrophage colony-stimulating factor
C; Keywords: Cytckine; 91ycoprotein; 91covth factor; macrophage
F; 1-32/Domain: signal sequence #status predicted cAMT>
F; 13-12/Binding site: carbohydrate (Asn) (covalent) #status predicted
R; Ladner, M.B.; Martin, G.A.; Noble, J.A.; Wittman, V.P.; Warren, M.K.; McGrogan, M.; Proc. Natl. Acad. Sci. U.S.A. 85, 6706-6710, 1988
A; Title: cDNA clonding and expression of murine macrophage colony-stimulating factor f A; Reference number: A31401; MUID:88320507; PMID:2457916
A; Reference number: A31401
A; Molecule type: MRNA
A; Residues: 1-52 < LAD>
A; Cross-references: GB:M21952; GB:J03862; NID:g192804; PIDN:AAA37481.1; PID:g309199
A; Cross-references: GB:M21952; GB:J03862; NID:g192804; PIDN:AAA37481.1; PID:g309199
A; Harrington, M.A.; Edenberg, H.J.; Saxman, S.; Pedigo, L.M.; Daub, R.; Broxmeyer, H. Gene 102, 165-170, 1991
A; Title: Cloning and characterization of the murine promoter for the colony-stimulatin A; Reference number: JN0294; MUID:91340149; PMID:1874443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 TKLLRFAVDREARLGQTPFP-----DVMEQVFHEVG----IGSVLSLQKFWQHRIK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E----KIDGTSTLREDHQEPGSPHIATPNPQRVSNSATPVAQLLLPKSH-----SWGI 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    354 VSGHGVLGSDVFEEPPMSG-----MSEAGI------PQSPDDSDSSYGSHSTDSL 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---IQAETDRPRALSASPFPKSTEDQKPVDITDRPLTEVNPMRPIGQT-----QNNTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 SSQTNRSSFDLLPREFRLVEVHDPPLHQPSANKPKPPTMLDIPSEPCSLTIHTIQLIQHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 SQRTEGSS--LLPSELPL-----RIEDPGSAKQRP-----PRSTCQ-TLESTEQPNHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 RRLRNLIATAQAQNQQQTEGVKTEESEPLPSCPGSPPLPDDLLPLDCKNPNAPFQIRHSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 -ESSL--GINWVLEEASGEASEGFLTQ------EAKFSPSTPVGGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.7%; Score 123; DB 1; Length 552; Best Local Similarity 21.6%; Pred. No. 0.29; Matches 90; Conservative 47; Mismatches 144; Indels 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               271 DRL-------TEDSQPHPSAGGPVPGVEDIL-----
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El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                             Gwinn, M.L.; Dodson, R.J
H.; Dragoi, I.; Sellers,
                                                                                                                                                                                                                                                                             hypothetical protein VC0998 [imported] - Vibrio cholerae (strain N16961 serogroup 01) C; Species: Vibrio cholerae C; Date: 18-Mug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C; Accession: A82255 R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, Nature 406, 477-483, 2000 A; Firser, C.M.
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A:Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- DALADAQLESATESEVESELELVSEPAAEEAFTELDELDFYTEEDALADSQLEPAA 1079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADAOLEPVAESEVEPELDLASE----- 1021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166
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         899 IGLIQGFLKKNLEEFGLDELLEDEDIRPRSKPPRPRPRPPNGKITTGR----KRIASSVFL 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EIPISSSQTNRSSFDLL----PREFRLVEVHDPPLHQPSANKPKPPTMLDIPSEPCSLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----DDLLPLDCKNPNAPFQIRHSDPESDFYRGKGEPVTELSWHSCRQLLYQAVA--TIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AHAGFDCANESVLETLTDVAHEYCLKFTKLLRFAVDREA - - RLGQTPFPDVMEQVFHEVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 IGSVLSLQKFWQHRIKDYHSYMLQISKQLSE----EYERIVNPEKATEDA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IHTIQLIQHNRRLRNL-IATAQAQNQQQTEGVKTEESEPLPSCPGSP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1621 <HEI>
A;Cross-references: GB.AE004181; GB.AE003852; NID:99655454;
A;Experimental source: serogroup 01; strain N16961; biotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.8%; Score 126; DB 2; I 21.7%; Pred. No. 0.85; tive 75; Mismatches 169;
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                                                                           NORCKKR 410
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NQSLRKK 961
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Best Local Similarity
Matches 93; Conserv
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Spore coat assembly protein (spovID) - Bacillus subtilis
C; Species: Bacillus subtilis
C; Species: Bacillus subtilis
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C; Accession: A69716; B47083
R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berr
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Pabret, C.; Ferrari,
Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
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Koetter, P.; Koningstein, G.; Krogh, S.; Knamano, M.; Kurita, K.; Lapidus, A.; Lardino
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
y, M.; Ogawa, K.; Ogiwarara, A.; Oudega, B.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
A; Authors: Voshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tata, K.; Yasauncto,
A; Witters, P.; Wipat, A.; Yamamaco, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Voshida
A; Witters: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A; Accession: A69716
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A; Residues: 1-575 < KUN>
A; Residues: 1-575 < KUN>
A; Cross-references: GB: A1009126; NID: 92635200; PIDN: CAB14771.1; PID: e11840
A; Cross-references: Strain 168
B; Beall, B.; Driks, A.; Losick, R.; Moran Jr., C.P.
J. Bacteriol. 175, 1709-1716, 1993
A; Title: Cloning and characterization of a gene required for assembly of the Bacillus A; Reference number: A47083; MUID: 93194796; PMID: 8449878
A; Accession: B47083
                                                                                    17;
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                                                                                                                                                                                                                                                                                        QAGQQQAQG--PPGYGPYGYAPQASTGYPPPPSQQSPY-APQAGPPPQMRHQYPPHSQQQ 241
                                                                                                                                                                                             PPPHYPSSNGPSQQGYRPGPVTNGPPPQGQYPPPP--QAPQNYQQMYHQQR-----AQQQ 184
                                                                                                                                                                                                                                                                                                                                                                    -----DFYRGKGEPVTELSWHSCRQLLYQAVATILAHAGFDCANESVLETLTDVAHEYC 190
                                                                                                                                                                                                                                                                                                                                                                                                                           281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 HRIKDYHSYMLQISKQLSE-EYERIVNPEKATEDAKPVKIKEEPVSDITFPVSEELEADL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           296 ASGDQSLPMGVLGAQSERFPSN---LEVEASPQASSAEVNASPLWNLAHVKMEPQESEEG 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --PPTMLDIPSEPCSLTIHTIQLIQHNRRLRNLIATAQ
                                                                                                                                                                                                                                                        85 AQNQQQTEGVKTEESEPLPSCP----GSPPLPDDLLPLDCKNPNAPFQIRHSDPES----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             353 NVSGHGVLGSD-----VFEEPMSGMSEAGIPQSPD-----DSDSSYGSHSTDSLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 LKFTKLLRFAVDREARLGOTPFPDVMEQVFH-----EVGIGSVLSLQKF-----WQ
                                                                                    127;
                                                                                                                                                                                                                                                                                                                                                                                                                        242 APPGYWDGYQGYGGPPPS-----QQQQQGGGPVTAPQSMQMAQQ----
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                                                                                    Indels
                                   Length
                          5.6%; Score 121.5; DB 2;
20.0%; Pred. No. 4.5;
Live 44; Mismatches 172;
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                                                                                    Conservative
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                             Query Match
Best Local Similarity
Matches 86; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----DVMEQVFHEVG----IGSVLSLQKFWQHRIK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 RRLRNLIATAQAQNQQQTEGVKTEESEPLPSCPGSPPLPDDLLPLDCKNPNAPFQIRHSD 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 PESDFYRGKGEPVTELSWHSCRQLLYQAVATILAHAGFDCANESVLETLTDVAHEYCLKF 193
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Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Natural 1999 #sequence_revision 10-Sep-1999
Cispecies: 10-Sep-1999 #sequence_revision 10-Sep-1999
Cispecies: Natural 1993 #sequence_revision 1993
Biochim. Biophys. Acta 1174, 143-152, 1993
A;Ritle: Isolation and characterization of a cDNA clone encoding for rat CSF
A;Ritle: Isolation and characterization of a cDNA clone encoding for rat CSF
A;Reference number: S35703
A;Retus: preliminary
A;Rocession: S35703
A;Status: preliminary
A;Residues: 1-552 <BNBA
A;Residues: 1-552 <BNBA
A;Cross-references: EMBL:M84361; NID:q203640; PIDN:AAA03032.1; PID:q203641
C;Superfamily: macrophage colony-stimulating factor
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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T33152
  -SSDPQIPESVFHLLVPGIILVLLTVGGLLFYKWKWRSHRDPQTLDSSVGRPEDSSL 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            354 VSGHGVLGSDVFEEPMSG----MSEAGI-----POSPDDSDSSYGSHSTDSL 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 SSQTNRSSFDLLPREFRLVEVHDPPLHQPSANKPKPPTMLDIPSEPCSLTIHTIQLIQHN
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A;Map position: 1
A;Introns: 122/3; 293/3; 515/3; 1205/2; 1577/1; 2221/3; 2776/1; 2864/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47; Mismatches 144; Indels 136;
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A; Accession: T28736
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A;Residues: 1-1332 csTE>
A;Residues: 1-1332 csTE>
A;Residues: 1-1332 csTE>
A;Cross-references: EMBL:235950; NID:9536341; PIDN:CAA85026.1; PID:9536342; MIPS:YBR081d
B;Andre, B.; C21epluch, C.; Hein, C.; Jauniaux, J.C.; Urrestarazu, A.; Vissers, S.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45893
A;Recession: S45948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 IL-AHAG-----FDCANESVL----ETLTDVAHEYCLKFTKLLRFAVDREARLGQT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           350 ADPALCOEEAEPDEALESVSEAALSIEDSRETASAVYMENDNADLHFHFNOKTSSEEASO 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KQLSEEYERIVNPEKATED---AKPVKIKEEPVSDITFPVSEELEADLASGDQSLPMGVL 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable transcription factor SPT7 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YBR0739; protein YBR081c
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 28-Jan-1994 #sequence_revision 09-Sep-1994 #text_change 20-Sep-1999
C;Accession: $41552; $45946; $45948; $40800; $45478; $54985; $59716
R;Gansheroff, L.; Dollard, C.; Tan, P.; Winston, F.
submitted to the EMBL Data Library, July 1993
A;Reference number: $41552
A;Reference number: $41552
                                                                                                                                                                                                                                                                                                                                                                  |: | : ::|| | :|:
----FISKAGLREELETE---KAESEPPESVASEPEAREDVKEEEESEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 LPLDCKNPNAPFQIRHSDPESD-----FYRGK---GEPVTELSWHSCRQLLYQAVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 PFPDV-MEQVFHEVGIGSV----LSLQK-----FWQHRIKDYHSYMLQ-----IS
                                                                                                                                                                                                                                 EIPISSSQTNRSSFDLLPREFRLVEVHDPPLH----QPSANKPKPPTML-DIPSEPCSLT
                                                                                                                                                                                                                                                                                                                                  64 IHTIQLIQHNRRLRNLIATAQAQNQQTEGVKTEESEPLPSCPGSPPLPDDL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Molecule type: DNA
A; Residues: 1-133 - GGAN-
A; Cross-references: EMBL-L22537; NID:g349189; PIDN:AAC37424.1; PID:g349190
R; Steensma, H.Y.; van der Aart, Q.J.M.
submitted to the Protein Sequence Database, August 1994
A; Reference number: 845932
A;Residues: 'MNL',2-575 <BEA>
Note: sequence extracted from NCBI backbone (NCBIN:127855, NCBIP:127857)
C;Genetics:
A;Gene: spoVID
                                                                                                                                                                                    Gaps
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A; Residues: 1-873 cAND>
A; Cross-references: EMBL:235950; MIPS:YBR081c
A; Cross-references: EMBL:235950; MIDS:YBR081c
R; Haypes, S.R.; Dollard, C.; Winston, F.; Beck, S.; Trowsdale, J.; Dawid,
Nucleic Acids Res. 20, 2603, 1992
                                                                                                                            ; Score 117; DB 2; Length 575;
; Pred. No. 0.85;
53; Mismatches 158; Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAQSERFPSNLEVEASPQASSAEVNASPLWNLAHVKMEPQESEEGN 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.4% Best Local Similarity 21.4% Matches 87; Conservative
                                                                                                                                                                                                                                                                                   146
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A; Secure and sequence not snown; translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-624, LRGKKRRI', 633-1332 <VAN>
A; Cross-references: EMBL:X76294
A; Cross-references: EMBL:X76294
A; Cross-references: EMBL:X76294
A; Cansheroff, L.J.: Dollard, C.; Tan, P.; Winston, F.
Genetics 139, 523-536, 1995
A; Title: The Saccharomyces cerevisiae SPT7 gene encodes a very acidic protein importa
A; Reference number: S54985; MUID:95229044; PMID:7713415
A; Accession: S54985
A; Status: nucleic acid sequence not shown
A; Residues: I-1332 <GAW>
A; Cross-references: EMBL:L22537; NID:9349189; PIDN:AAC37424.1; PID:9349190
B; Van der Aart, O.J.M.
Submitted to the EMBL Data Library, August 1995
A; Reference number: S59702
A; Accession: S59702
A; Accession: S59702
A; Accession: S59702
A; Accession: S59702
                                  R; van der Aart, Q.J.M.; Barthe, C.; Doignon, F.; Aigle, M.; Crouzet, M.; Steensma, H. Yeast 10, 959-964, 1994
A; Title: Sequence analysis of a 31 kb DNA fragment from the right arm of Saccharomyce A; Reference number: $45462; MUID: 95076715; PMID: 7985423
A; Reference number: $45478
A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: DNA
A;Residues: 1-1332 <VRAW>
A;Residues: 1-1332 <VRAW>
A;Cross-references: EMBL:X76294; NID:g974203; PIDN:CAA53940.1; PID:e264674; PID:g5583
A;Experimental source: strain $288C
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Caenorhabditis elegans
C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 NPNAPFQIRH-----SDPESDFYRGKGEPVTELSWHSCR-----QLLYQAVATILAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      940 NPNA-FLNNHIYNYTIIDDSLDI-----DPVSQLPTHDYKNNRELIWKFMHKNISKVAMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 LSLQKFWQHRIKDYHSYM------LQISKQLSEEYER-IVNP-----EKATEDAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1050 -----nrpddlfsyvesefgkktkklodikoklesflrallrptloelsernfedes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272 PVKIKEEPVSDIT----FPVSE-ELEADLASGDQSLPMGVLGAQSERFPSNLEVEASPQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 AGFDCANESVLETLTDVAHEYCLKFTKLLRFAVDREARLGQTPFPDVMEQVFHEVGIGSV
A;Cross-references: EMBL;M87651; NID:g172683; PIDN:AAA35087.1; PID:g172684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 2R
C;Superfamily: unassigned bromodomain proteins; bromodomain homology
C;Keywords: nucleus; transcription regulation
F;466-521/Domain: bromodomain homology <BRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              327 SSAEVNASPLWNLAHVKMEPQESEEGNVSGHGVLGSDVFEEPMSGMSEAG 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1332;
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R; Sammons, L.; Wohldmann, P.; Beck, C.
submitted to the EMBL Data Library, September 1997
A; Description: The sequence of C. elegans cosmid F26G5.
A; Reference number: Z20516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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Best Local Similarity 21.4%; Pred. No. 6.4;
Matches 62; Conservative 49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: SGD:SPT7
A;Cross-references: SGD:S0000285; MIPS:YBR081c
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A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-609 <sam> A;Cross-references: EMBL:AF022974; PIDN:AAC48035.1; GSPDB:GN00023; CESP:F26G5.1 A;Experimental source: strain Bristol N2; clone F26G5 C;Genetics: A;Gene: CESP:F26G5.1 A;Map position: 5 A;Introns: 59/1; 140/1; 540/1</sam>	Db 354 DQETYLTAN Qy 145 -PVTELSWH	DQETYLTANRHGVSDQQYDSMAKTMNS-FQTTTIRHPMPLIATTNATGSNTSGTSASIIR 412         -PVTELSWHSCRQLLYQAVATILAHAGFDCANESVLETLTDVAHEYCLKFTKLLRFA 200
Query Match 5.1%; Score 112; DB 2; Length 609; Best Local Similarity 21.6%; Pred. No. 2.2; Matches 77; Conservative 47; Mismatches 149; Indels 84; Gaps 15;	Qy 243HSYMLQIS   :   :   Db 512 DIQSVLKQNNPS	HSYMLQIS KQLSEEYERIVN
QY 75 RLENLIATAQAQNQQTEGV-KTEESEPLPSCPGSPPLFDDLLPLDCKNPNAPFQIRHSD 133   ::  :	Qy 263PEKP   1   572 NNKIIPNNS	PEKATEDAKPVKIKEEPVSDITFPVSEELEADLASGDQSLPMGVLGA 309   :   :   :       :     :         :
QY 134 PESDFYRGKGEPVTELSWHSCRQL-LYQAVATILAHAGFDCANESVLETLTDVAHEYCLK 192  Db 144 SRVDLPRKPAPPADHSNKELPLKSSKSEIREGGNQAATQHIQESL 189	Qy 310 QSERFPSNI :    Db 632 SPLSYPRNI	OSERFPSNLEVEASPQASSAEVNASPLWNLAHVKMEPQESEEGNV
. QY 193 FTKLLRFAVDREARLGGTPFPDVMEQVFHEVGIGSVLSLQKFWQHRIKDYHSYMLQ 248 :   :   :	Qy 355Db 691 SASHSKWSF	SEAGVLGSDVFEEPMSGMSEAGIPQSPDD 383 
QY 249ISKQLSEEYERIVNPEKATEDAKPVKIKEEPVSDITFPVSEELEADLASGDQ 300  232 PTSVIDKALRCLFERRISQKSDPTKSLQDVPETVNQPEIAFFNSLPQSIIDHYE 285	Qy 384 SDSSYGSHG :: 1   1   1   1   1   1   1   1   1   1	SDSSYGSHSTDSLM-GSSPVFNQ 405 ::
QY 301 SLPMGVLGAQSERFPSNLEVEASPQASSAEVNASPLWNLAHVKMEPQESEEGNVSGH 357 :	RESULT 10 S53407	
Qy 358 GVLGSDVFEEPMSGMSEAGIPQSPDDSDSSYGSHSTDSLMGSSPVFNQRCKRNMRKI 414. : :: :	CHS5 protein - yeast (S N;Alternate names: prot C;Species: Saccharomyce C;Date: 05-May.1995 #se C;Accession: S53407	accharomyces cerevisiae) ein L8543.18; protein YLR330w s cerevisiae quence_revision 01-Sep-1995 #text_change 19-Apr-2002
RESULT 9 S54016 SOK2 protein - yeast (Saccharomyces cerevisiae) N;Alternate names: protein YM9711.03c; protein YMR016c C;Species: Saccharomyces cerevisiae C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 06-Feb-1998	R;Du, Z. submitted to the EMBL I A:Description: The seq. A;Reference number: S5:A A:Accession: S53407 A;Molecule type: DMA A;Residues: 1-671 < DUZ>	R;Du, z. submitted to the EMBL Data Library, Pebruary 1995 A;Description: The sequence of S. cerevisiae cosmid 8543. A;Reference number: S53390 A;Reference number: Market S53300 A;Reference number: A;Reference number: A;Reference number: A;Reference number: A;Reference number: A;Reference number: A;Residues: 1-671 < DUZ>
1	A;Cross-references: EME A;Experimental source: C;Genetics: A;Genetics: A;Cross-references: SGI A;Map position: 12R	L:U20618; NID:92258165; PIDN:AAB64526.1; PID:9662142; GSPDB:GN strain S288C (AB972) CAL3; MIPS:YLR330w ::S0004322
A; Residues: 1-785 <lye> A; Cross-references: EMBL: Z49211; NID: g798922; PID: g798925; MIPS: YMR016c A; Experimental source: strain AB972 C; Genetics:</lye>	Query Match Best Local Similarity Matches 76; Conser	5.0%; Score 108.5; DB 2; Length 671; .larity 20.5%; Pred. No. 4.6; Conservative 53; Mismatches 159; Indels 83; Gaps 15;
references: SGD:S0004618; Sition: 13R	Oy 79 LIATAQAQA   1	LIATAQAQNQQOTEGVKTEESEPLPSCPGSPPLPDDLLPLDCKNPNAPFQIR 130    :
Query Match 5.1%; Score 110.5; DB 2; Length 785; Best Local Similarity 18.8%; Pred. No. 4.1; Matches 106; Conservative 67; Mismatches 189; Indels 201; Gaps 24;	131	
QY 8 GEIPISSSQTNRSSFDLLPREFRLVEVHDPPLHQPSANKPKPPTMLDI 55   : :: :           SAMSPNSNRTSRNSNSISSLAQQPPMSNYPQPSTYQYPQFHKTSSIPNSHSPIPPRSLTT 306	184	GQTPFPDVMEQVFHEVGIGSVLSLQKFWQHR
QY 56 PSEPCSLTIHTIQLIQHNRRLRNLIATAQAQNQQCTEGVKTEESEPLPSCPGS 108   ::	239	FPVSEELEADL
QY 109 PP1PDDLLPLDCKNPNAPFQIRHSDPESDFYRGKGE144 :	296	

us-09-857-308-1.rpr

	Db 712 INIHSENTENKGEMGALPKPETILPPEPENGKGNDTDSGTGSTVENSSDL 762
352 GNVSGHGVLGSDVFEEPMSGMSEAGIPQSPDDSDSSYGSHSTDSLMGSSPV 402	NLSISSFLSKTKDSGSVSLQETRRQKKTLKK
403 FNQRCKRRMRK 413 ::    :  657 NKKNKRNKKK 667	RESULT 12 T26216 hypothetical protein W06A7.3c - Caenorhabditis elegans C;Species: Caenorhabditis elegans
RESULT 11 protein kinase SK2 - rat protein kinase SK2 - rat C; Species: Rattus norvegicus (Norway rat) C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C; Accession: 714021 R; Fukami, Y: Yamamoto, H.; Ichihara, T.; Mori, K.; Gomi, T.; Sato, K. submitted to the EMBL Data Library, April 1997	#text_change 15-Oct-1999
A; Description: SK2, a putative rat homologue of yeast protein kinase NRK1. A; Reference number: 221463 A; Reference number: 221463 A; Accession: T34021 A; Accession: T34021 A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-1206 < FWL> A; Residues: 1-1206 < FWL> A; Residues: EMBL: AB003357; NID: d1106513; PID: d1020890; PIDN: BAA20077.1 A; Experimental source: strain SD	A;Cross-references: EMBL:278066; PIDN:CAB51467.1; GSPDB:GN00023; CESP:W06A7.3c A;Experimental source: clone W06A7 C;Genetics: A;Gene: CESP:W06A7.3c A;Map position: 5 A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2 Query Match 4.9%; Score 107; DB 2; Length 2484;
i; (2 itch 5.0%; Score 108.5; DB 2; Length 1206; :al Similarity 20.3%; Pred. No. 11;	<pre>Best Local Similarity 19.2%; Pred. No. 42; Matches 85; Conservative 70; Mismatches 168; Indels 120; Gaps 28 EFRLVEVHDPPLHQPSANKPKPPTMLDIPSEPCSLTIHTIQLIQHNRRLRNLIATAQAQN</pre>
6 YMGEIPISSSQTNRSSFDLLPREFRLVEVHDPPLHQPSANKPKPPT 51	DD 1368 COLOVATVEFELESABEESEATEVOEPLEXVEVOPDLS.OSPAHILIDLEHRIPKDH 1427
52 MLDIPSEPCSLTIHTIQLIQHNRRLRNLIATAQAQ 86 : ::	
87 NQQOTEGVKTEESEPLP	QY 166 LAHAGFDCANESVLETLTDVAHEYCLKFTKLLRFAVDREARLGGTPFPDVMEQ 218
104	QY 219 VFHEVGIGSVLSLQKFWQHRIKDYHSYMLQISKQLSEEYERIVNPEKATEDAKPVKIK 276 :: ::         ::       Db 1544ATWYLEEWVEWIIADAVKEVSEMEVVTESEISEMAPQVSESTC 1586
148 ELSWHSCRQLLYQAVATILAHAGFDCANESVLETLTDVAHEYCLKFTKLLRFAVDR 203	QY 277EEPVSDITFPVSEELEADLASGDQSLPMGVLGAQSERFPSNLEVEASP324   1   1   1   1   1   1   1   1   1
204EARLGQT-PFPDV	Qy 325QASSAEVNASPLWNLAHVKMEPQESEEGNVSGHGVLGSDVFEEPMSGMS 373   1   1   1   1   1   1   1   1   1
241 DYHSYMLQISKQLSE	Qy 374 EAGIPQSPDSDSSYGSHSTDSL 396 
VKIKEEPEADLASGDQSLP:	RESULT 13 T26215 hypothetical protein W06A7.3a - Caenorhabditis elegans
304MGVLGAQSERFPSNLEVEASPQASSAEVNASPLWNLAHVKMEPQ 347	elegans nce_revision 15-Oct-1 Library, August 1996
	acabau

A; Accession: T26215 A; Status: preliminary; translated from GB/EMBL/DDBJ	:  :
A; Residues: 1-2607 <wil> A; Residues: 1-2607 <wil> A; Cross-references: EMBL: 278066; PIDN: CAB01522.2; GSPDB: GN00023; CESP: W06A7.3a A; Experimental source: clone W06A7</wil></wil>	QY 133 DPESDFYRCKGEPVTELSWHSCRQLLYQAVATILAHAGFDCANESVLETLTDVAHEYCLK 192 1
A;Gene: CESP:W06A7.3a A;Map position: 5 A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2; 2586/2	QY 193 FTKLLRFAVDREARLGGTPFPDVMEQVFHEVGIGSVLSLQKFWQHRIKDYHSYMLQISKQ 252
Query Match 4.9%; Score 107; DB 2; Length 2607; Best Local Similarity 19.2%; Pred. No. 45; Matches 85; Conservative 70; Mismatches 168; Indels 120; Gaps 20;	QY 253 LSEEYERIVNPEKATEDAKPVKIKEEPVSDITFPVSEELEADLASGDQSLPMGV 306   1   1   1   1   1   1   1   1   1
QY 28 EFRLVEVHDPPLHQPSANKPKPPTMLDIPSEPCSLTHTIQLIQHNRRLRNLIATAQAQN 87	QY 307LGAQSERFPSNLEVEASPQASSAEVNASPLWNLAHVKMEPQESEGGNVSGHGVLGSD 363
QY         88         QQ	Qy 364 VFEEPMSGMSEAGIPQSPDDSDSSYGSHSTD 394    :
Qy 119 -DCKNPNAPFQIRHSDPESDFYRGKGEPVTELSWHSCRQLLYQAVATI 165	RESULT 15 T20773
	hypothetical protein ZK270.2c - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999 C;Accession: T20773; T27816
OY 219 VPHEVGIGSVLSLQKFWQHRIKDYHSYMLQISKQLSEEYERIVNPEKATEDAKPVKIK 276  DD 1544ATMYLEEMVEWIIADAVKRVSE-MEVVYRESEISBWAPOVSESTC 1586	R;Kershaw, J. Submitted to the EMBL Data Library, November 1996 A;Reference number: 219322 A;Accession: T20773
	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-180 <will)< td=""></will)<>
325QASSAEVNASPLWNLAHVKMEPQESEEGNVSGHGVLGSDVFEEPMSGMS 1   1   1   1   1   1   1   1   1   1	vember 1996
374 EAGIPQSPDSDSSYGSHSTDSL 396	A; Meterence number: 420423 A; Accession: T27816 A; Status: preliminary; translated from GB/EMBL/DDBJ A: Molocule type: DNA
Db 1691 QQKPPEKPTEDIGALSPNTL 1713 RESULT 14	A; Residues: 1-1180 <w12> A; Residues: 1-1180 <w12> A; Cross-references: EMBL: 282089; PIDN: CABO5005.1; GSPDB: GN00019; CESP: ZK270.2c A; Experimental source: clone ZK270</w12></w12>
A43704 involucrin - western tarsier c:Species: Tarsius bancanus (western tarsier)	A;Gene: CESP:ZK270.2c A;Map position: 1 A;Introns: 933/3; 974/3; 1008/2; 1100/3; 1151/3
, ,	Query Match 4.9%; Score 106; DB 2; Length 1180; Best Local Similarity 19.9%; Pred. No. 16; Matches 94; Conservative 51; Mismatches 177; Indels 150; Gaps 19;
A;TLLE: INVOLUCTIN gene of tarsloids and other primates: alternatives in evolution of the A;Reference number: A43704; MUID:91271381; PMID:1905021 A;Accession: A43704 A;Status: translation not shown	QY 23 DLLPREFRLVEVHDPPLHQPSANKPRPPTMLDIPSEPCSLTIHT 66
A; Residues: 1-387 < DIS A CALIS A; Residues: 1-387 < DIS A CALIS A; Cross-references: GB:M65124; NID:g343451; PIDN:AAA36960.1; PID:g343452 C; Comment: During the terminal differentiation of keratinocytes, this protein from the californ and a protein from the calibration of the	QY 67 IQLIQHNRRLRNLIATAQAQNQQQTEGVKTEESEPLPSCPGSPPLPDDLL 116   1   1   1   1   1   1   1   1   1
C; Superfamily: involucrin C; Keywords: cornified cell envelope; duplication; epidermis; tandem repeat	Qy 117 PLDCKNPNAPFQIRHSDPESDFYRGKGEPVTELSWHSCRQLLYQAVATIL 166
Ouery Match 4.9%; Score 106; DB 1; Length 387; Best Local Similarity 23.0%; Pred. No. 3.1; Matches 76; Conservative 37; Mismatches 140; Indels 78; Gaps	TPFPDVMEQVFH       :   KPEAYGFSSDVYTGSLN
QY 77 RNLIATAQAQNQQQTEGVKTEESEPLPSCPGSPPLPDDLLPLDCKN-PNAPFQIRHS 132	

77 RNLIATAQAQNQQQTEGVKTEESEPLPSCPGSPPLPDDLLPLDCKN-PN---APFQIRHS 132

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qa	432 SDSGSPKKDDKDKGFRFRFSKASPKSSGYPEVSPTFEGPIDVTGRVESLE 482
Οy	309AQSERFPSNLEVEASPQASSAEVNASPLWNLAHVKMEPQESEEGNVSGHGVLG 361
qq	483 HVPLQSREFPTYSPRKSQEKPSEKSSERTVEPKRYHLIARIRHEGDEETVENPDTYG-FA 541
Qy	GSSPVF
qq	542 STSYDGPLEETSKSVDVEETPISVSNVYHHGESIRUEKRQRK 584

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July 18, 2003, 07:48:47; Search time 91.237 Seconds (without alignments) 604.643 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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2175
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human ART-1 protei	Human protein segu	Human cell death p	Gene 41 human secr	Human secreted pro	Human cell death p	Human cell death p	Human endometrium	Human cell death p	Human cell death p
SUMMARIES	AAB03880	. AAM25845	AAG98644	AAB45216	AAB45217	AAG98646	AAG98652	AAY59941	AAG98654	AAG98656
DB	21	22	22	21	21	22	22	20	22	22
Length	414	419	412	403	404	363	199	198	169	111
% Query Match Length DB	100.0	100.0	99.1	97.5	94.7	87.3	47.0	42.1	39.4	26.3
Score	2175	2175	2155	2121	2059.5	1898	1022	915	828	572
Result No.	1	7	m	4	2	9	7	<b>&amp;</b>	6	10

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	⋖	18 AAW35752 18 AAW22615 21 AAB19547 21 AAY90329 22 AAE00546	22 AAAB3900 23 AAB49459 22 ABB69480 22 ABB69480 21 AAW43338 21 AAY54041	4	AAB1954 AAY9033 AAE0054 AAB5960 AAB4946
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bound cytotoxic T cell; tumour; cancer; remedy; prevent; diagnose. Human; tumour antigen protein; ART-1; HLA antigen; cytostatic; AAB03880 standard; protein; 414 AA Human ART-1 protein sequence. 98JP-0341253. 99WO-JP06682. 26-OCT-2000 (first entry) WO200032770-A1 Homo sapiens. 30-NOV-1999; 01-DEC-1998; 08-JUN-2000. AAB03880; AAB03880 

ALIGNMENTS

(SUMU ) SUMITOMO PHARM CO LTD. (ITOH/) ITOH K. WPI; 2000-412318/35. N-PSDB; AAA62864. Itoh K, Gomi S;

Novel tumor antigen protein ART-1, tumor antigen peptide originating from it, their derivatives, and DNAs, applicable in vivo or in vitro as  ${\sf res}$ 

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                                                                  Included in the invention are polynucleotide sequences encoding the ART-1 protein, and muteated ART-1 proteins which when broken down intracellularly produce a tumour antigen peptide that can recognise HLA antigen and bound cytotoxic T cells. Antibodies which specifically recognise ART-1 and its derivative peptides, are also included in the invention. ART-1 exhibits cytostatic activity. The tumour antigen protein, tumour antigen peptide originating from it, their derivatives, and DNAs are applicable in vivo or in vitro as remedies, preventives and
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                                                      The invention relates to a novel human tumour antigen protein, ART-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnostics for tumours. The present sequence represent sequence
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                                                                                                                                                                                                                                                 100.0%; Score 2175; DB 21; Length 414; 100.0%; Pred. No. 1.4e-191; de 0; Mismatches 0; Indels 0;
 remedies, preventives and diagnostics for tumors
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                            59pp; Japanese.
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es 414; Conservative
                            Page 44-46;
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AAM25965. The proteins can have activities based on the tissues and cells they are expressed in, such as: antinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; cardiart; immunosuppressive; antibacterial; endocrine; cardiant; cardiant; cardiant; antianaemic; antiaggregant; harmostatic; unlinerary; antidiabetic; cytostatic; eneuroprotective; antidepressant; nootropic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; cardiant; and polynucleotides are useful for screening for production, The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, cancemia, disease, parkinson's disease, neurodegenerative and neurological disorders.
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                                Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated human polynucleotides encoding polypeptides, useful for treatment and diagnosis of e.g. cancer, ulcers and HIV infection
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allergic rhinitis; diabetes; multiple sclerosis; depression;
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100.0%; Pred. No. 1.4e-191;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                        99US-0471275.
2000US-0488725.
2000US-0552317.
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                                                                   neurological disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAH99786
                                                                                                                                                                                          WO200153455-A2
                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                           21-JAN-2000;
25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                  23-DEC-1999;
                                                                                                                                                                                                                                                    26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang YT,
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SLPMGVLGAQSERFPSNLEVEASPQASSAEVNASPLWNLAHVKMEPQESEEGNVSGHGVL 360
                                                                                 Sequences AAH84132-AAH84370 represent human nucleic acid sequences which protect against cell death (i.e., apoptosis or necrosis). Sequences AAH84131, AAH84145, AAH84140, AAH84210, AAH84216, AAH84315 and AAH8430 represent 10 full-length cons. While the remaining nucleic acid sequences within the range given above represent the open reading frames (ORFS) of these cDNA clones. Sequences AAG98610-AAG98829 represent the polypeptides encoded by the cell death protective ORFs. The cell death protective cDNA clones are able to prevent, delay or reverse progression through the apoptotic or necrotic pathways when injected into a cell predisposed to or undergoing cell death. The cell death protective nucleic acids and polypeptides can be used in the diagnosis and treatment of disorders associated with cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell death protective; apoptosis; necrosis; human; drug screening; cell death-associated disorder; central nervous system disorder; psychiatric disorder; neurological disorder; ischaemia-related disorder; stroke; cerebral infarction; ischaemic encephalopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neurodegenerative disorder: Alzheimer's disease; Huntington's disease; Parkinson's disease; Infection; meningitis; malaria; trypanosomiasis; vascular disease; opthalmological disorder; diabetic retinopathy; macular degeneration; hypertension; myocardial infarction; atherosclerosis; respiratory disorder; asthma; transgenic animal; chronic obstructive pulmonary disease; neoplastic condition; cancer; benign tumour; anaemia; agarcointestinal disorder; gastriits; ulcerative colitis; liver disease; biliary cirrhosis; kidney disorder; glomerulonephritis; cystitis; endomertnic disorder; drawe's disease; Hashimoto's thyrolditis; skin condition; dermatitis; urticaria; immune disorder; acquired immunodeficiency syndrome; ADDS.
                                                                                                                                                                                                                                                                                                                                                                                                        Human cell death protective cDNA clone CNI-00714 ORF1 protein, SEQ:77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel protective sequence polynucleotides and polypeptides, used to identify modulators of their expression and activity, which are used to treat central nervous system conditions, diseases and disorders -
                                                                                                                                          GSDVFEEPMSGMSEAGIPQSPDDSDSSYGSHSTDSLMGSSPVFNQRCKKRMRKI 414
                                                                                                                                                                  Barney S, Thomas MB, Portbury SD, Puranam K, Katz LC;
                                                                                                                                                                                                                                                                                     AAG98644 standard; Protein; 412 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-DEC-2000; 2000WO-US33547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0461697.
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cath, and to screen for compounds which modulate their activity or expression. Such modulators, preferably a small organic molecule, an antibody, a ribozyme, or an antisense molecule, can also be used to treat cell death-related diseases. Such diseases include those associated with the central nervous system including psychiatric or neurological disorders, especially ischaemia-related conditions such as strokes, and also includes neurodegenerative disorders such as Alzheimer's disease, Huntington's disease, or Parkinson's disease. The modulators may also be used to treat infections such as meningitis, malaria, or trypanosomiasis; vascular diseases such as ischaemic encephalopathy or cerebral infarction; eye conditions such as asthma or chronic obstructive pulmonary disease, neoplastic conditions such as carbona or chronic obstructive pulmonary disease, neoplastic conditions such as cancers or benign tumours; blood cell conditions such as asthma or chronic obstructive as conditions such as cancers or benign tumours; blood cell conditions such as asthma or chronic obstructive orditis; liver conditions such as asthma conditions such as allower clirkosis; kidney disorders such as glomerulonephritis; cystitis; endometriosis; endocrine disorders such as glomerulonephritis; or immune thyroiditis; such as dermatitis or uniquental conditions conditions such as dermatitis or uniquental conditions conditions such as dermatitis or uniquental conditions and as dermatitis or uniquental conditions conditions such as dermatical conditions or conditions and as dermatitis or uniquental conditions conditions and as dermatical conditions or conditions and as dermatitis or uniquental conditions and as as a condition conditions and as a c ö 124 184 244 242 304 302 364 Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; creebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; cancer; opthalmalogical; autoimmune disease; hyperproliferative disorder; 64 62 system disorders such as acquired immunodeficiency syndrome (AIDS). The nucleic acids may additionally be used to generate animal models of cell death-associated disorders. The present sequence represents a 3 RYWGEIPISSSQTNRSSFDLLPREFRLVEVHDPPLHQPSANKPKPPTMLDIPSEPCSLTI HTIQLIQHNRRLRNLIATAQAQNQQQTEGVKTEESEPLPSCPGSPPLPDDLLPLDCKNPN APFQIRHSDPESDFYRGKGEPVTELSWHSCRQLLYQAVATILAHAGFDCANESVLETLTD 185 VAHEYCLKFTKLLRFAVDREARLGQTPFPDVMEQVFHEVGIGSVLSLQKFWQHRIKDYHS 245 YMLQISKQLSEEYERIVNPEKATEDAKPVKIKEEPVSDITFPVSEELEADLASGDQSLPM 305 GVLGAQSERFPSNLEVEASPQASSAEVNASPLWNLAHVKMEPQESEEGNVSGHGVLGSDV 5 RYWGEIPISSSQTNRSSFDLLPREFRLVEVHDPPLHQPSANKPKPPTMLDIPSEPCSLTI Gaps Gene 41 human secreted protein homologous amino acid sequence #157. FEEPMSGMSEAGIPQSPDDSDSSYGSHSTDSLMGSSPVFNQRCKKRMRKI 412 .; 0 FEEPMSGMSEAGIPQSPDDSDSSYGSHSTDSLMGSSPVFNQRCKKRMRKI 414 Length 412; Indels 99.1%; Score 2155; DB 22; 100.0%; Pred. No. 9.8e-190; iive 0; Mismatches 0; AAB45216 standard; Protein; 403 AA. cell death protective polypeptide. (first entry) Best\_Local Similarity 100. Matches 410; Conservative 412 AA; 12-FEB-2001 AAB45216; 63 243 365 Sequence Query Match AAB45216 ΟŻ g ò g Óλ 셤 ò g δ g ò g ŏ q 

us-09-857-308-1.rag

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Polynucleotide sequences AAC80531-C80580 represent cDNA encoding human secreted proteins AAB45120-B45169. Sequences AAB45170-B45255 represent alternative polypeptides encoded by the genes, and amino acid sequences to which they are homologous. The genes and proteins have activities to dependent on the tissues and cells in which they are expressed. Examples of their activities include immunosuppressive; antiarthritic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; and opthalmalogical. The secreted proteins, polynucleotides, antiagonists and agonists may be useful in treating, preventing and/or diagnosist and agonists may be useful in treating, preventing and/or diagnosing diseases and disorders such as autoimmune diseases of the breast or liver, cardiovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. corneal infections caused by cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Albeimer's disease, infections caused by corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotraxis. The polypeptides can also be used to aid wound healing and epithelial cell proliferation and coular disorders e.g. corneal infection also be used as a food additive or preservative to increase or decrease cused in the isolation and characterisation of the genes and proteins of the increase and proteins of
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                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's Parkinson's diseases and cancers -
cardiovascular disorder; cerebrovascular disorder; wound healing;
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                   nervous system disorder; aging; chemotaxis
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99US-0172410.
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                                                                                                                                                                    2000WO-US07505.
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Best Local Similarity 100.0
Matches 403; Conservative
                                                                                                                                                                                                                                                                                                 Ruben SM,
                                                                                                                                                                                                                                                                                                                                    WPI; 2000-611712/58.
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                                                       Homo sapiens.
                                                                                                                                                                    22-MAR-2000;
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Polynucleotide sequences AAC80531-C80580 represent cDNA encoding human secreted proteins AAB45120-B45169. Sequences AAB45170-B4525 represent alternative polypeptides encoded by the genes, and amino acid sequences to which they are homologous. The genes and proteins have activities cof their activities include immunosuppressive; antiarthritic; of their activities include immunosuppressive; antiarthritic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; and opthalmalogical. The secreted proteins, polynucleotides, antagonists and agonists may be useful in treating, preventing and/or diagnosing diseases and disorders such as autoimmune diseases of neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders such as autoimmune diseases of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. carebral isohaemia, angiogenesis, nervous system disorders e.g. carebral isohaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by the polypeptides can also be used to aid wound healing and epithelial cells to proliferation, to prevent skin aging due to sunburn, to maintain control of the proliferation, to prevent skin aging due to sunburn, to maintain
                                     300
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; norotropic; neuroprotective; antibacterial; virucide; fungicide; cancer; opthalmalogical; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; aging; chemotaxis.
304
245 YMLQISKQLSEEYERIVNPEKATEDAKPVKIKEEPVSDITFPVSEELEADLASGDQSLPM
                    Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -
                                                                             GVLGAQSERFPSNLEVEASPQASSAEVNASPLWNLAHVKMEPQESEEGNVSGHGVLGSDV
                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein sequence encoded by gene 41 SEQ ID NO:158.
                                                                                                                                                                                    FEEPMSGMSEAGIPQSPDDSDSSYGSHSTDSLMGSSPVFNQRC 407
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                                                                                                                                                                                                                                                                                                     AAB45217 standard; Protein; 404 AA
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99US-0172410.
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17-DEC-1999;
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organs before transplantation, for supporting cell culture of primary

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HTIQLIQHNRRLRNLIATAQAQNQQQTEGVKTEESEPLPSCPGSPPLPDDLLPLDCKNPN 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell death protective; apoptosis; necrosis; human; drug screening; cell death-associated disorder; central nervous system disorder; psychiatric disorder; neurological disorder; ischaemia-related disorder;
tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAC8622-C80530 and AAB45119 represent sequences used in the isolation and characterisation of the genes and proteins of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stroke; cerebral infarction; ischaemic encephalopathy; neurodegenerative disorder; Alzheimer's disease; Huntington's disease; Parkinson's disease; infection; meningitis; malaria; trypanosomiasis; vascular disease; opthalmological disorder; diabetic retinopathy; macular degeneration; hypertension; mycoardial infarction; atherosclerosis; respiratory disorder; asthma; transgentc animal; chronic obstructive pulmonary disease; neoplastic condition; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ulcerative colitis; liver disease; biliary cirrhosis; kidney disorder; glomerulonephritis; oystitis; endometritosis; endocrine disorder; Grave's disease; Hashimoto's thyroiditis; skin condition; dermatitis; urticaria; immune disorder; acquired immunodeficiency syndrome, AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAHEYCLKFIKLLRFAVDREARLGQTPFP-DVMEQVFHEVGIGSVLSLQKFWQHRIKDYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGVLGAQSERFPSNLEVEASPQASSAEVNASPLWNLAHVKMEPQESEEGNVSGHGVLGSD
                                                                                                                                                                                                                                                                                                                       APFQIRHSDPESDFYRGKGEPVTELSWHSCRQLLYQAVATILAHAGFDCANESVLETLTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cell death protective cDNA clone CNI-00714 ORF3 protein, SEQ:81
                                                                                                                                                                                         RYWGEIPISSSQINRSSFDLLPREFRLVEVHDPPLHQPSANKPKPPTMLDIPSEPCSLTI
                                                                                                                                                             Gaps
                                                                                                                             Length 404;
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                                                                                                                            Score 2059.5; DB Pred. No. 6e-181; 2; Mismatches
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                                                                                                                             94.7%;
98.0%;
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                                                                                                                                                             Conservative
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                                                                                              404 AA;
                                                              the invention.
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                                                                                              Sequence
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                                                                                                                            Query Match
Best Local
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CC AAH84132, AAH84170, AAH84201, AAH84210, AAH84256, AAH84182, AAH84145, AAH84170, AAH84201, AAH84226, AAH84165, AAH84170, AAH84201, AAH84201, AAH84185, AAH84170, AAH84201, AAH84201, AAH84185, AAH84170, AAH84201, AAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              endometriosis; endocrine disorders such as Grave's disease or Hashimoto's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequences AAH84132-AAH84370 represent human nucleic acid sequences which
                                                                                                                                                                                                                                                                                                                 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease, neoplastic conditions such as cancers or benign tumours; blood cell conditions such as anaemia; gastrointestinal conditions such as gastritis or ulcerative colitis; liver conditions such as biliary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thyroiditis; skin conditions such as dermatitis or urticaria; or immune system disorders such as acquired immunodeficiancy syndrome (AIDS). The nucleic acids may additionally be used to generate animal models of cell death-associated disorders. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MLDIPSEPCSLTIHTIQLIQHNRRLRNLIATAQAQNQQQTEGVKTEESEPLPSCPGSPPL
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                                                                                                                                                                                                                                                                                   Novel protective sequence polynucleotides and polypeptides, used to identify modulators of their expression and activity, which are used to treat central nervous system conditions, diseases and disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MLDIPSEPCSLTIHTIQLIQHNRRLRNLIATAQAQNQQQTEGVKTEESEPLPSCPGSPPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kidney disorders such as glomerulonephritis; cystitis;
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                                                                                                                                                        Puranam K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; DB 22;
3.9e-166;
                                                                                                                                                     Portbury SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.3%; Score 1898; D
100.0%; Pred. No. 3.9
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                    (COGE-) COGENT NEUROSCIENCE INC.
                                                                                                                                                     Thomas MB,
11-DEC-2000; 2000WO-US33547.
                                                                                                                                                                                                                                  N-PSDB; AAH84170, AAH84173.
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Best Local Similarity 100.
Matches: 363; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 6C; 325pp;
                                                                                                                                                                                                         2001-390297/41.
                                                                                                                                                        Barney S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     363 AA;
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181 QKFWQHRIKDYHSYMLQISKQLSEEYERIVNPEKATEDAKPVKIKEEPVSDITFPVSEEL 240
                              351
                                                                                  411
                                                                                               Sequences AAH84132-AAH84370 represent human nucleic acid sequences which AAH84121. AAH84130. Sequences halfalatoric against cell death (i.e., apoptosis or necrosis). Sequences AAH84213. AAH84150. AAH84220. AAH84226. AAH84256. AAH84201. AAH84215. AAH84315 and AAH84367 represent 10 full-length cDNA clones, while the remaining nucleic acid sequences within the range given above represent the open reading frames (ORFs) of these cDNA clones. Sequences AAG98610-AAG98829 represent the polypeptides encoded by the cell death protective cDNA clones are able to prevent, delay or reverse progression through the apoptotic or necrotic
                                                                                                                                                                                                                                                                                                                                                           cell death-associated disorder; central nervous system disorder; psychiatric disorder; neurological disorder; ischaemia related disorder; stroke; cerebral infarction; ischaemic encephalopathy; neurodegenerative disorder; Alzheimer's disease; Huntington's disease; Parkinson's disease; infection; meningitis; malaria; trypanosomiasis; vascular disease; opthalmological disorder; diabetic retinopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                           macular degeneration; hypertension; myocardial infarction; atherosclerosis; respiratory disorder; asthma; transgenic animal; chronic obstructive pulmonary disease; neoplastic condition; cancer; benign tumour; anaemia; gastrointestinal disorder; gastritis; ulcerative colitis; liver disease; biliary cirrhosis; kidney disorder; glomerulonephritis; oystitis; endometrisosis; endocrine disorder; grave's disease; Hashimoto's thyroiditis; skin condition; dermatitis; urticaria; immune disorder; acquired immunodeficiency syndrome; AIDS.
                           Human cell death protective cDNA clone CNI-00714 ORF9 protein, SEQ:93.
                                                                                GNVSGHGVLGSDVFEEPMSGMSEAGIPQSPDDSDSSYGSHSTDSLMGSSPVFNQRCKKRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel protective sequence polynucleotides and polypeptides, used to identify modulators of their expression and activity, which are used to treat central nervous system conditions, diseases and disorders -
                                                                                                                                                                                                                                                                                                                                                 death protective; apoptosis; necrosis; human; drug screening;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Puranam K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thomas MB, Portbury SD,
                                                                                                                                                                                                                                      AAG98652 standard; Protein; 199 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 6I; 325pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (COGE-) COGENT NEUROSCIENCE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0461697.
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                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lo DC, Barney S,
                                                                                                                                                      ||||
RKI 363
                                                                                                                                      RKI 414
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                                                                               352
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                                                                                                                                                                                                          RESULT 7
AAG98652
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death. The cell death protective nucleic and polypeptides can be used in the diagnosis and treatment of disorders associated with cell death. The cell death protective nucleic and polypeptides can be used in the diagnosis and treatment of disorders associated with cell death. The construction of antibody, a ribozyme, or an antisense molecule, can also be used to treat cell death-related diseases. Such diseases include those associated with the central nervous system including psychiatric or neurological disorders, especially ischaemia-related conditions such as Alzheimer's disease, thutington's disease, or Parkinson's disease. The modulators may also be used to treat infections such as meningitis, malaria, or trypanosomiasis, wasculat diseases such as isofhaemic encephalopathy or erebral.

Consideration: eye conditions such as asthma or chronic obstructive pulmonary disease; neoplastic conditions such as asthma or chronic obstructive pulmonary disease; neoplastic conditions such as cannot estimate the conditions such as cannot conditions such as cannot can benign tumours; blood cell conditions such as asthma or chronic obstructive pulmonary disease; neoplastic conditions such as cannot estimate the sease or Hashimoto's cirrhosis; kidney disorders such as agencers or benign tumours; or immune contities; or immune contities; or immune continistics or integrals or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             system disorders such as acquired immunodeficiency syndrome (AIDS). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216 MEQVFHEVGIGSVLSLQKFWQHRIKDYHSYMLQISKQLSEEYERIVNPEKATEDAKPVKI
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         predisposed to or undergoing cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 199;
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100.0%; Pred. No. 8.4e-86;
ive 0; Mismatches 0;
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pathways when injected into a cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98DE-1017948.
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Matches 199; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DE19817948-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell death
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY59941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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that are highly expressed in therine theory (LDMA) sequences (A) that are highly expressed in therine theory (LDMA) sequences (B) and anticancer and cytostatic activity. (A) are used (1) for recombinant expression of polypeptides (B) and (ii) to isolate complete genes. (B) are used (1) to identify agents suitable for treatment of uterine or (including expression from gene therapy vectors) and (iii) for generation of specific antibodies. (A) are identified by assembling ESTS (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTS from different libraries may represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  different parts of the same unknown gene, distorting the estimated trequency of occurrence in a particular tissue. AAY59941-Y60328 represent protein fragments encoded by the human endometrium tumour cDNA library derived EST fragments represented in AAZ41981-242121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLITHTIQLIQHNRRLRNLIATAQAQNQQQTEGVKTEESEPLPSCPGSPPLPDDLLPLDC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 KNPNAPFQIRHSDPESDFYRGKGEPVTELSWHSCRQLLYQAVATILA-HAGFDCANESVL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell death protective; apoptosis; necrosis; human; drug screening; cell death-associated disorder; central nervous system disorder; psychiatric disorder; neurological disorder; ischaemia-related disorder; stroke; cerebral infarction; lschaemic encephalopathy; neurodegenerative disorder; Alzheimer's disease; Huntington's disease; Parkinson's disease; infection; meningtis; malaria; trypanosomiasis; vascular disease; opthalmological disorder; diabetic retinopathy; macular degeneration; hypertension; myocardial infarction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cell death protective cDNA clone CNI-00714 ORF11 protein, SEQ:97.
                                          <u>ы</u>
                                                                                                                                                                                                                                                                   This invention describes novel human nucleic acid (cDNA) sequences (A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MNLQRYWGEIPISSSQTNRSSFDLLPREFRLVEVHDPPLHQPSANKPKPPTMLDIPSEPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 MNLQRYWGEIPISSSQTNRSSFDLLPREFRLVEVHDPPLHQPSANKPKPPTMLDIPSEPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      derived polypeptides, for treatment of uterine and endometrial cancer and identification of therapeutic agents \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atherosclerosis; respiratory disorder; asthma; transgenic animal; chronic obstructive pulmonary disease; neoplastic condition; cancer;
                                          Dahl
                                                                                                                                             nucleic acid sequences expressed in uterine cancer tissues, and
                                          Pilarsky C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                          Schmitt A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 6.1e-76;
1; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 915;
(META-) METAGEN GES GENOMFORSCHUNG MBH.
                                        Hinzmann B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG98654 standard; Protein; 169 AA.
                                                                                                                                                                                                                          Claim 23; Page 275; 444pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 42.1%;
Best Local Similarity 91.6%;
Matches 175; Conservative
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                                        Specht T,
                                                                               WPI; 1999-591957/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 AA;
                                                                                                    N-PSDB; AAZ41981.
                                      Rosenthal A,
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                                                                                                                                             New
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death, and to screen for compounds which modulate their activity or expression. Such modulators, preferably a small organic molecule, an antibody, a ribozyme, or an antisense molecule, can also be used to treat cell death-related diseases. Such diseases include those associated with the central nervous system including psychiatric or neurological disorders, especially ischaemia-related conditions such as strokes, and also includes neurodegenerative disorders such as Alzheimer's disease, Huntington's disease, or Parkinson's disease. The modulators may also be used to treat infections such as meningitis, malaria, or trypanosomiasis; vascular diseases such as ischaemic encephalopathy or cerebral infarction; eye conditions such as diabetic retinopathy or macular degeneration; hypertension; myocardial infarction; atherosclerosis; respiratory conditions such as asthma or chronic obstructive pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        endometriosis; endocrine disorders such as Grave's disease or Hashimoto's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protect against cell death (i.e., apoptosis or necrosis). Sequences AAH84132, AAH84131, AAH84135, AAH84201, AAH84201, AAH84205, AAH84205, AAH84205, AAH84205, AAH84201, AAH84131, AAH84135, AAH84201, CDNG clones, while the remaining nucleic acid sequences within the range given above represent the open reading frames (ORFS) of these cDNA clones. Sequences AAG98010-AAG98029 represent the polypeptides encoded by the cell death protective cDNA clones are able to prevent, delay or reverse progression through the apoptotic or necrotic pathways when injected into a cell predisposed to or undergoing cell death, The cell death protective nucleic acids and polypeptides can be used in the diagnosis and treatment of disorders associated with cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences AAH84132-AAH84370 represent human nucleic acid sequences which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease; neoplastic conditions such as cancers or benign tumours; blood cell conditions such as anaemia gastrointestinal conditions such as gastritis or ulcerative colitis; liver conditions such as billary cirrhosis; kidney disorders such as glomerulonephritis; cystitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   skin conditions such as dermatitis or urticaria; or immune
benign tumour; anaemia; gastrointestinal disorder; gastritis; ulcerative colitis; liver disease; biliary cirrhosis; kidney disorder; glomerulonephritis; cystitis; endometricosis; endocrine disorder; Grave's disease; Hashimoto's thyroiditis; skin condition; dermatitis; urticaria; immune disorder; acquired immunodeficiency syndrome; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel protective sequence polynucleotides and polypeptides, used to identify modulators of their expression and activity, which are used to treat central nervous system conditions, diseases and disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   system disorders such as acquired immunodeficiency syndrome (AIDS). nucleic acids may additionally be used to generate animal models of cell death-associated disorders. The present sequence represents a cell death protective polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Katz LC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Puranam K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thomas MB, Portbury SD,
                                                                                                                                                                                                                                                                                                                                                                                                                         (COGE-) COGENT NEUROSCIENCE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 6K; 325pp; English.
                                                                                                                                                                                                                                                                                                                     11-DEC-2000; 2000WO-US33547.
                                                                                                                                                                                                                                                                                                                                                                      99US-0461697.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barney S,
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                                                                                                                                                                                                               WO200145638-A2
                                                                                                                                                                                                                                                                                                                                                                      14-DEC-1999;
                                                                                                                                                                 Homo sapiens.
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ВС,
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Gaps

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Length 169; Indels

39.4%; Score 858; DB 22; 100.0%; Pred. No. 8.5e-71; iive 0; Mismatches 0;

Best Local Similarity 100. Matches 169; Conservative

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Query Match

246 MIQISKQLSEEYERIVNPEKATEDAKPVKIKEEPVSDITFPVSEELEADLASGDQSLPMG 305

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61 VLGAQSERFPSNLEVEASPQASSAEVNASPLWNLAHVKMEPQESEGNVSGHGVLGSDVF 120
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  1 MLQISKQLSEEYERIVNPEKATEDAKPVKIKEEPVSDITFPVSEELEADLASGDQSLPMG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell death protective; apoptosis; necrosis; human; drug screening; cell death-associated disorder; central nervous system disorder; psychiatric disorder; neurological disorder; ischaemia-related disorder; stroke; cerebral infarction; ischaemic encephalopathy; neurodegenerative disorder; Alzhehmer's disease; Huntington's disease; Parkinson's disease; infection; meningitis; malaria; trypanosomiasis; vascular disease; opthalmological disorder; diabetic rethnopathy; atherosclerosis; respiratory disorder; asthma; transgenic animal; ethenic obstructive pulmonary disease; neoplastic condition; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cell death protective cDNA clone CNI-00714 ORF13 protein, SEQ:101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel protective sequence polynucleotides and polypeptides, used to identify modulators of their expression and activity, which are used in to treat central nervous system conditions, diseases and disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             benign tumour; anaemia; gastrointestinal disorder; gastritis; ulcerative colitis; liver disease; biliary cirrhosis; kidney disorder; glomerulonephritis; cystitis; endometricosis; endocrine disorder; Grave's disease; Hashimoto's thyroiditis; skin condition; dermatitis; urticaria; immune disorder; acquired immunodeficiency syndrome; AIDS.
                                             306 VLGAQSERFPSNLEVEASPQASSAEVNASPLWNLAHVKMEPQESEEGNVSGHGVLGSDVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Katz LC;
                                                                                                                                                               121 EEPMSGMSEAGIPQSPDDSDSSYGSHSTDSLMGSSPVFNQRCKKRMRKI 169
                                                                                                                                       366 EEPMSGMSEAGIPQSPDDSDSSYGSHSTDSLMGSSPVFNQRCKKRMRKI 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thomas MB, Portbury SD, Puranam K,
                                                                                                                                                                                                                                                                                                  AAG98656 standard; Protein; 111 AA
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N-PSDB; AAH84170, AAH84183.
                                                                                                                                                                                                                                                                                                                                                                                              21-SEP-2001 (first entry)
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AAG98656
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Librardes, representative disease, conditions such as Alzheimer's disease, the national conditions such as meningitis, malaria, or trypanosomiasis; used to treat infections such as meningitis, malaria, or trypanosomiasis; vascular diseases such as ischaemic encephalopathy or cerebral infarction; eye conditions such as diabetic retinopathy or macular degeneration; hypertension; myocardial infarction; atherosclerosis; respiratory conditions such as asthma or chronic obstructive pulmonary disease, neoplastic conditions such as cancers or benign tumours; blood cell conditions such as anaemia; gastrointestinal conditions such as anaemia; gastrointestinal conditions such as cancers or paniary cirrhosis; kidney disorders such as glomerulonephritis; cystitis; endometriosis; endocrine disorders such as glomerulonephritis; or stitis; chyroiditis; skin conditions such as dermatitis or urticaria, or immune system disorders such as dermatitis or urticaria, or immune system disorders such as dermatitis or urticaria, or immune call dash associated disorders. The present sequence represents a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell dath-associated disorder; central nervous system disorder; stroke; cerebral infarction; ischemic nercophalopathy; stroke; cerebral infarction; ischemic necephalopathy; stroke; cerebral infarction; ischemic necephalopathy; neurodegenerative disorder; Alzahamer's disease; Huntington's disease; parkinson's disease; infection; meningitis; malaria; trypanosomiasis; vascular disease; opthalmological disorder; diabetic retinopathy; macular degeneration; hypertension; myocardial infarction; atherosclerosis; respiratory disorder; asthma; transgenic animal; chronic obstructive pulmonary disease; neoplastic condition; cancer; benign tumour; anaemia; gastrointestinal disorder; gastritis; ulcerative colitis; liver disease; billary cirrhosis; kidney disorder; grave's disease; Rashimoto's thyroiditis; skin condition; dermatitis; urticaria; immune disorder; acquired immunodeficiency syndrome; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGVLGAQSERFPSNLEVEASPQASSAEVNASPLWNLAHVKMEPQESEEGNVSGHGVLGSD 60
                  antibody, a ribozyme, or an antisense molecule, can also be used to trea cell death-related diseases. Such diseases include those associated with the central nervous system including psychiatric or neurological disorders, especially ischaemia related conditions such as strokes, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
expression. Such modulators, preferably a small organic molecule, an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 VFEEPMSGMSEAGIPQSPDDSDSSYGSHSTDSLMGSSPVFNQRCKKRMRKI 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 VFEEPMSGMSEAGIPQSPDDSDSSYGSHSTDSLMGSSPVFNQRCKKRMRX 111
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.3%; Score 572; DB 22; Length 111; 100.0%; Pred. No. 1e-44; 1ve 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell death-associated disorders. vicell death protective polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG98658 standard; Protein; 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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99US-0461697.

14-DEC-1999;

cell death-associated disorder; central nervous system disorder; psychiatric disorder; neurological disorder; ischaemia-related disorder;

stroke; cerebral infarction; ischaemic encephalopathy;

death protective; apoptosis; necrosis; human; drug screening;

neurodegenerative disorder; Alzheimer's disease; Huntington's disease; Parkinson's disease; infection; meningitis; malaria; trypanosomiasis; vascular disease; opthalmological disorder; diabetic retinopathy; macular degeneration; hypertension; myocardial infarction; atheroscierosis; respiratory disorder; asthma; transgenic animal; chronic obstructive pulmonary disease; neoplastic condition; cancer; benign tumour; anaemia; gastrointestinal disorder; gastritis;

in

Katz LC;

Puranam K,

ulcerative colitis; liver disease; biliary cirrhosis; kidney disorder; glomerulonephriths; oystitis; endometriosis; endocrine disorder; Grave's disease; Hashimoto's thyroiditis; skin condition; dermathits; urticaria; immune disorder; acquired immunodeficiency syndrome; AIDS.

Katz LC;

Barney S, Thomas MB, Portbury SD, Puranam K,

Lo DC,

N-PSDB; AAH84170, AAH84189. WPI; 2001-390297/41.

(COGE-) COGENT NEUROSCIENCE INC.

99US-0461697.

14-DEC-1999;

11-DEC-2000; 2000WO-US33547.

WO200145638-A2.

28-JUN-2001

Homo sapiens.

Human cell death protective cDNA clone CNI-00714 ORF19 protein, SEQ:113

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Sequences AAH84132-AAH84370 represent human nucleic acid sequences which
                                                                                                                                               protect against cell death (i.e., apoptosis or necrosis). Sequences AAH84132, AAH84145, AAH84170, AAH84201, AAH84210, AAH84226, AAH84281, AAH84315 and AAH84367 represent 10 full-length cDNA clones,
                                                                            Novel protective sequence polynucleotides and polypeptides, used to identify modulators of their expression and activity, which are used to treat central nervous system conditions, diseases and disorders -
                             Barney S, Thomas MB, Portbury SD,
                                                                                                                    Claim 1; Fig 60; 325pp; English.
          (COGE-) COGENT NEUROSCIENCE INC.
                                               WPI; 2001-390297/41.
N-PSDB; AAH84170, AAH84185.
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; 0 0; Indels 17.1%; Score 371; DB 22; 100.0%; Pred. No. 1.7e-26; 100.0%; Preu. ... 71; Conservative Similarity 71 AA; Sequence Query Match Local Matches

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404 NORCKKRMRKI 414

NORCKKRMRKI 71 61

AAG98662 standard; Protein; 46 AA. AAG98662; RESULT 12 AAG98662 AX SX EX

21-SEP-2001 (first entry)

cirrhosis; kidney disorders such as glomerulonephritis; cystitis; endometriosis; endocrine disorders such as Grave's disease or Hashimoto's thyroiditis; skin conditions such as dermatitis or urticaria; or immune system disorders such as acquired immunodeficiency syndrome (AIDS). The

while the remaining nucleic acid sequences within they converge with the range given above represent the open reading frames (ORES) of these CDNA clones. Sequences AAG98610-AAG98829 represent the polypeptides encoded by the cell death protective CDNA clones are able to protective ORES. The cell death protective cDNA clones are able to prevent, delay or reverse progression through the apoptotic or necrotic pathways when injected into a cell predisposed to or undergoing cell death. The cell death protective nucleic acids and polypeptides can be used in the diagnosis and treatment of disorders associated with cell eath, and to screen for compounds which modulate their activity or expression. Such modulators, preferably a small organic molecule, an antibody, a ribozyme, or an antisense molecule, can also be used to treat antibody, a ribozyme, or an antisense molecule, can also be used to treat cell death-related diseases. Such diseases include those associated with the central nervous system including psychiatric or neurological disorders, especially ischaemia-related conditions such as strokes, and also includes neurodegenerative disorders such as Alzheimer's disease, Huntington's disease, or Parkinson's disease. The modulators may also be used to treat infections such as meningitis, malaria, or trypanosomiasis; vascular diseases such as ischaemic encephalopathy or cerebral infarction; eye conditions such as diabetic retinopathy or macular degeneration; hypertension; myocardial infarction; atherosclerosis; respiratory conditions such as asthma or chronic obstructive pulmonary disease; neoplastic conditions such as cancers or benign tumours; blc cell conditions such as anaemia; gastrointestinal conditions such as gastritis or ulcerative colitis; liver conditions such as biliary cirrhosis; kidney disorders such as glomerulonephritis; cystitis; system disorders such as acquired immunodeficiency syndrome (AIDS). nucleic acids may additionally be used to generate animal models of cell death-associated disorders. The present sequence represents a cell death protective polypeptide. system disorders such as acquired

endometriosis; endocrine disorders such as Grave's disease or Hashimoto's thyroiditis; skin conditions such as dermatitis or urticaria; or immune

protect against cell death (i.e., apoptosis or necrosis). Sequences hich protect against cell death (i.e., apoptosis or necrosis). Sequences AAH84132, AAH84132, AAH84126, AAH84210, AAH84210, AAH842110, AAH84211, AAH8 Novel protective sequence polynucleotides and polypeptides, used to identify modulators of their expression and activity, which are used in to treat central nervous system conditions, diseases and disorders vascular diseases such as ischaemic encephalopathy or cerebral infarction; eye conditions such as diabetic retinopathy or macular degeneration; hypertension; myocardial infarction; atherosclerosis; respiratory conditions such as asthma or chronic obstructive pulmonary disease; neoplastic conditions such as cancers or benign tumours; blo cell conditions such as anaemia; gastrointestinal conditions such as gastritis or ulcerative colitis; liver conditions such as biliary Claim 1; Fig 6S; 325pp; English. 344 MEPQESEEGNVSGHGVLGSDVFEEPMSGMSEAGIPQSPDDSDSSYGSHSTDSLMGSSPVF 403 Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell death protective; apoptosis; necrosis; human; drug screening; cell death-associated disorder; central nervous system disorder; psychiatric disorder; neurological disorder; ischaemia related disorder; stroke; cerebral infarction; ischaemic encephalopathy; neurodegenerative disorder; Alzheimer's disease; Huntington's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cell death protective cDNA clone CNI-00714 ORF20 protein, SEQ:115.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parkinson's disease; infection; meningitis; malaria; trypanosomiasis; vascular disease; opthalmological disorder; diabetic retinopathy; vascular degeneration; hypertension; myocardial infarction; macular degeneration; hypertension; myocardial infarction; atherosclerosis; respiratory disorder; asthma; transgenic animal; chronic obstructive pulmonary disease; neoplastic condition; cancer; benign tumour; anaemia; gastrointestinal disorder; gastritis; ulcerative colitis; liver disease; biliary cirrhosis; kidney disorder; glomerulonephritis; cystitis; endometricosis; endocrine disorder; grave's disease; Hashimoto's thyroiditis; skin condition; dermatitis; urticaria; immune disorder; acquired immunodeficiency syndrome; AIDS.
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                                                                                                                                                                Gaps
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additionally be used to generate animal models of
                    cell death-associated disorders. The present sequence represents a cell death protective polypeptide.
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                                                                                                                                                                                                    369 MSGMSEAGIPQSPDDSDSSYGSHSTDSLMGSSPVFNQRCKKRMRKI 414
                                                                                                                                                                                                                        Length 46;
                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Puranam K,
                                                                                                                      Score 239; DB 22;
Pred. No. 1.3e-14;
                                                                                                        11.0%; Sco...
100.0%; Pred. No....
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                         AAG98663 standard; Protein; 43 AA.
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                                                                                                                    Query Match 11.0
Best Local Similarity 100.
Matches 46; Conservative
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nucleic acids may
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                                                                               46 AA;
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                                                                                                                                                                                                                                                                                                                                                                                 AAG98663;
                                                                               Sequence
                                                                                                                                                                                                                                                                                                   RESULT 13
AAG98663
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death. The cell death protective nucleic and polypeptides can be used in the diagnosis and treatment of disorders associated with cell death. The cell death protective nucleic and polypeptides can be catch. The diagnosis and treatment of disorders associated with cell each. The and to screen for compounds which modulate their activity or expression. Such modulators, preferably a small organic molecule, an antibody, a ribozyme, or an antisense molecule, can also be used to treat cell death-related diseases. Such diseases include those associated with the central nervous system including psychiatric or neurological disorders, especially ischaemia related conditions such as strokes, and also includes neurodegenerative disorders such as Alzheimer's disease, the modulators may also be used to treat infections such as meningitls, malaria, or trypanosomiasis; or sacular diseases such as inchaemic encephalopathy or macular degeneration; hypertension; myocardial infarction; atherosclerosis; cepiratory conditions such as asthma or chronic obstructive pulmonary disease; neoplastic conditions such as asthma or chronic obstructive pulmonary cell conditions such as an anemia; gastrointestinal conditions such as asthma conditions such as asthma conditions such as asthma conditions such as astences or benign tumours; blood cell conditions such as astences or benign tumours; blood cell conditions such as astences or benign tumours; blood cell conditions such as an an antice conditions such as an and an antice conditions such as an a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cirrhosis, Kidney disorders such as glomerulonephritis; cystitis; endocrine disorders such as Grave's disease or Hashimoto's endometriosis; endocrine disorders such as Germatitis or urticaria; or immune system disorders such as acquired immunodeficiency syndrome (AIDS). The nucleic acids may additionally be used to generate animal models of cell death-associated disorders. The present sequence represents a cell death protective polypeptide.
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pathways when injected into a cell predisposed to or undergoing cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372 MSEAGIPOSPDDSDSSYGSHSTDSLMGSSPVFNQRCKKRMRKI 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSEAGIPQSPDDSDSSSYGSHSTDSLMGSSPVFNQRCKKRMRKI 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.3%; Score 224; DB 22;
100.0%; Pred. No. 2.8e-13;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB62430 standard; Protein; 359 AA.
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11-JUL-2000; 2000US-0614150.
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Matches 43; Conservative
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                                                                                                                                                                                                                     12;
                                     is
                                                                                                                                                                                                                                                                                         63 TIHTIQLIQHNRRLRNLIATAQAQNQQQTEGVKTEESEPLPSCPGSPPLPDDLLPLDCKN 122
                                                                                                                                                                                                                                                                                                                                         123 PNAPFQI---RHSDP-----ESDFYRGKGEPVTELSWHSCRQLLYQAVATILAHAGFD 172
                                                                                                                                                                                                                                                                                                                                                         DCSESAVQLLTDATEEFLRSFIGEYRGYYDSQPRLQNS---TVLQLVPLERAHFAQTGT- 218
                                                                                                                                                                                                                                                                                                                                                                                                                                        283
                                                                                                                                                                                                                                                                                                                 58 VIQTIEVMKQTEVLQSLIETYSNKN----GSSNYLLNPCLMIP-----EVDEPP 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SATGSSQSIGGMAMGDMLQDLG------GSTGSSGTVSSQQMLYGLLDGQ 322
                                                                                                                                                                                                                                                           WIPO
                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Prosophila. The invention useful in developmental biology and in elucidating cell sipaniling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                        173 CANESVLETLTDVAHEYCLKFTKLLRFAVDREARLGQTPFPDVMEQV-----FHEVGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                        SVLSLQKFWQHRIKDYHSYMLQISKQLSEEYERIVNPEKATEDAKPVKIKEEP---VSDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFPVSEELEADLASGDQSLPMGVLGAQSERFPSNLEVEASPQASSAEVNASPLWNLAHVK
                                                                                                                                                                                                                                          6 YWGEIPISSSQTNRSSFDLLP---REFRLVEVHDPPLHQPSANKPKPPTMLDIPSEPCSL
                                                                                                                                                                                                                    Gaps
                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                    64;
Disclosure; SEQ ID NO 14082; 21pp + Sequence Listing; English.
                                                                                                                                                                                           1. 6.1%; Score 132; DB 22; Length 359; Similarity 18.7%; Pred. No. 0.0022; 11; Conservative 71; Mismatches 174; Indels 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 2943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB58717 standard; Protein; 1049 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEPQESEEGNVSGHGVLGSD 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISSNTSNMTGTSGNGSTGGN 342
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2000US-0614150.
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticidaes, therapeutics and pharmaceutical frugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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19.1%; Pred. No. 0.015;
ative 71; Mismatches 174; Indels 132;
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## STIC SEARCH RESULTS FEEDBACK FORM

## Biotech-Chem Library

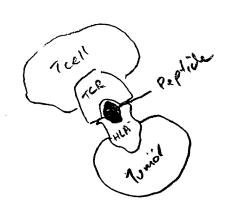
Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

Voluntary Results Feedback Form
> I am an examiner in Workgroup: Example: 1610
> Relevant prior art <b>found</b> , search results used as follows:
102 rejection
☐ 103 rejection
☐ Cited as being of interest.
☐ Helped examiner better understand the invention.
Helped examiner better understand the state of the art in their technology.
Types of relevant prior art found:
☐ Foreign Patent(s)
Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
> Relevant prior art <b>not found:</b>
Results verified the lack of relevant prior art (helped determine patentability).
Results were not useful in determining patentability or understanding the invention.
Comments:

Drop off or send completed forms to STIC/Blotech-Chem Library CLM - Circ. Desk





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